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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:56:34 ; Search time 33.8462 Seconds
(without alignments)
39.370 Million cell updates/sec

Title: US-09-632-748-4
Perfect score: 57
Sequence: 1 CVGSNGAIC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	57	100.0	10	AAW45346	Peptide used for d
2	57	100.0	10	AA199233	Cyclic peptide use
3	57	100.0	10	AA199233	Human beta-amyloid
4	57	100.0	10	AA199233	Beta-amyloid p75NTR
5	39	68.4	8	AA199233	Beta-amyloid fragm
6	39	68.4	8	AA199233	Human beta-amyloid
7	39	68.4	8	AA199233	Beta-amyloid pepti
8	39	68.4	8	AA199233	Human APP derived
9	39	68.4	10	AA199233	Human APP derived
10	39	68.4	10	AA199233	Human APP derived

11	39	68.4	10	22	AA199233	Human APP derived
12	39	68.4	11	23	AA199233	Human beta-amyloid
13	39	68.4	14	22	AA199233	Amyloid beta-prote
14	39	68.4	14	22	AA199233	Amyloid beta-prote
15	39	68.4	14	22	AA199233	Amyloid beta-prote
16	39	68.4	24	22	AA199233	Amyloid beta-prote
17	39	68.4	24	22	AA199233	Amyloid beta-prote
18	39	68.4	26	19	AA199233	Beta-amyloid pepti
19	39	68.4	26	20	AA199233	Human amyloidogeni
20	39	68.4	26	22	AA199233	Partial sequence o
21	39	68.4	27	20	AA199233	Human amyloidogeni
22	39	68.4	32	22	AA199233	Partial sequence o
23	39	68.4	33	20	AA199233	Synthetic amyloid
24	39	68.4	33	23	AA199233	Human beta-amyloid
25	39	68.4	35	17	AA199233	Beta-amyloid pepti
26	39	68.4	35	19	AA199233	Beta-amyloid pepti
27	39	68.4	35	20	AA199233	Beta-amyloid pepti
28	39	68.4	35	20	AA199233	Beta-amyloid pepti
29	39	68.4	35	20	AA199233	Beta-amyloid pepti
30	39	68.4	35	20	AA199233	Beta-amyloid pepti
31	39	68.4	35	22	AA199233	Amyloid beta-prote
32	39	68.4	35	22	AA199233	Amyloid beta-prote
33	39	68.4	35	23	AA199233	EEVHHHQQ-beta am
34	39	68.4	36	20	AA199233	Synthetic amyloid
35	39	68.4	38	15	AA199233	Beta-amyloid (1-38
36	39	68.4	38	20	AA199233	Human tachykinin a
37	39	68.4	38	22	AA199233	Amyloid beta-prote
38	39	68.4	38	22	AA199233	Amyloid beta-prote
39	39	68.4	39	15	AA199233	Beta-amyloid (1-39
40	39	68.4	39	20	AA199233	Human amyloid beta
41	39	68.4	39	20	AA199233	Synthetic amyloid
42	39	68.4	39	21	AA199233	Human Receptor to
43	39	68.4	40	14	AA199233	Beta-amyloid pepti
44	39	68.4	40	15	AA199233	Beta-amyloid (1-40
45	39	68.4	40	18	AA199233	Amyloid beta prote

ALIGNMENTS

RESULT 1
AAW45346
ID AAW45346 standard; peptide; 10 AA.
XX AAW45346;
AC AAW45346;
XX
DT 08-MAY-1998 (first entry)
XX
DE Peptide used for diagnosing and treating Alzheimer's disease.
XX
KW Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment;
KW neurotrophin receptor p75; p75NTR; nerve growth factor; NGF.
XX
OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 1..10 /note= "disulphide bond"
FT
XX
PN WO9737228-A1.
XX
PD 09-OCT-1997.
XX
PF 28-MAR-1997; 97WO-US04966.
XX
PR 29-MAR-1996; 96US-0625765.
XX
PA (UYBO-) UNIV BOSTON.
XX
PI Gilchrist BA, Yaar M;
XX
DR WPI; 1997-512306/47.

XX Evaluating risk of individual to develop Alzheimer's - uses cultured
 PT epidermal melanocyte(s), also useful for developing therapies for
 PT neuro-degenerative diseases
 XX
 PS Claim 14; Page 21; 42pp; English.
 XX
 CC The invention relates to methods of therapy for Alzheimer's disease
 CC using peptides (AAW45343-6) that bind to the neurotrophin receptor p75
 CC nerve growth factor receptor (NGFR) and competitively inhibit the binding
 CC of a beta-amyloid to the p75 NGFR. Also described is a new method for
 CC evaluating the risk of an individual to develop Alzheimer's disease
 CC using cultured neural crest-derived melanocytes. The methods can be used
 CC for diagnosing and treating Alzheimer's disease and other
 CC neurodegenerative diseases mediated by beta-amyloid protein, or by
 CC aberrant activation of the low affinity NGFR localised on neural cell
 CC surfaces, such as autoimmune encephalomyelitis, Huntington's disease,
 CC cortico-basal degeneration, progressive supra-nuclear palsy,
 CC Gerotman-Shaustler Scheinker syndrome, Niemann-Pick disease, and
 CC progressive supranuclear palsy. In the diagnostic tests, the human
 CC melanocytes, which are easily obtainable from skin biopsies, are good
 CC model cells for the study and diagnosis of Alzheimer's disease.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 18; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVGSNKGATC 10
 |||||
 Db 1 CVGSNKGATC 10

RESULT 2
 AAY39233
 ID AAY39233 standard; peptide; 10 AA.
 XX
 AC AAY39233;
 XX
 DT 23-NOV-1999 (first entry)
 XX
 DE Cyclic peptide used to inhibit p75-NTR mediated apoptosis.
 XX
 KW Cyclic peptide; p75NTR; p75 neurotrophin receptor; nerve growth factor;
 KW NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid;
 KW Alzheimer's disease; pseudo-ligand; hair growth; hair colour;
 KW skin colour; alopecia areata; male pattern baldness.
 XX
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Modified-site 1
 FT /note= "N-terminus is attached via a peptide bond to
 FT the C-terminus amino acid at position 10"
 FT
 FT Modified-site 10
 FT /note= "C-terminus is attached via a peptide bond to
 FT the N-terminus amino acid at position 1"

XX W09939728-A2.
 XX
 PD 12-AUG-1999.
 XX
 XX
 PF 03-FEB-1999; 99WO-US02362.
 XX
 XX 04-FEB-1998; 98US-0018194.
 XX
 XX (UYBO-) UNIV BOSTON.
 PA
 XX Eller M, Gilchrist BA, Yaar M;
 PI
 XX WPI; 1999-539950/45.
 DR
 XX

PT Controlling or manipulating melanocyte and keratinocyte cell death,
 PT useful for treating, e.g. alopecia areata
 XX
 PS Claim 4; Page 39; 67pp; English.
 XX
 CC This sequence is a cyclic peptide which competes with and competitively
 CC inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR).
 CC p75NTR is a low affinity nerve growth factor (NGF) receptor which is
 CC expressed by melanocytes and keratinocytes of the basal epidermis.
 CC Apoptosis can be inhibited by p75NTR via the upregulation of the Bcl-2
 CC protein. If the receptor is occupied by appropriate ligands e.g.
 CC neurotrophins, apoptosis is inhibited. Other examples of appropriate
 CC ligands include this cyclic peptide. This peptide is based on the
 CC sequence of the binding fragment of beta-amyloid, which binds to
 CC p75NTR in Alzheimer's disease. This cyclic peptide can be used in
 CC methods to control or manipulate keratinocyte or melanocyte cell death.
 CC The methods involve using this peptide or peptides AAY39234-Y39235 to
 CC bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting
 CC apoptosis. The new method can induce or maintain hair growth, hair colour
 CC or skin colour. Inducing or maintaining hair growth is useful for
 CC treating alopecia areata or male pattern baldness in vertebrates.
 XX
 SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVGSNKGATC 10
 |||||
 Db 1 CVGSNKGATC 10

RESULT 3
 AAG64004
 ID AAG64004 standard; peptide; 10 AA.
 XX
 AC AAG64004;
 XX
 DT 31-AUG-2001 (first entry)
 XX
 DE Human beta-amyloid-derived cyclic peptide #2.
 XX
 KW Human; beta-amyloid; nootropic; neuroprotective; anticonvulsant;
 KW p75 nerve growth factor receptor; inhibitor; Alzheimer's disease;
 KW neurodegenerative disease; cyclic.
 XX
 OS Homo sapiens.
 OS Synthetic.

XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..10
 FT /note= "the peptide has a cyclic structure as a
 FT result of the bonding between the two
 FT cysteine residues"

XX US6242416-B1.
 XX
 PD 05-JUN-2001.
 XX
 XX 29-SEP-1998; 98US-0163095.
 XX
 XX 29-MAR-1996; 96US-0625765.
 PR
 PR 28-MAR-1997; 97WO-US04966.
 XX
 XX (UYBO-) UNIV BOSTON.
 PA
 XX Gilchrist BA, Yaar M;
 PI
 XX WPI; 2001-380482/40.
 DR
 XX

XX Inhibition of beta-amyloid binding to the p75 nerve growth factor
 PT receptor using polypeptides, useful in the diagnosis and treatment of

PT e.g. Alzheimer's disease -
 XX
 PS Claim 2; Column 18; 16pp; English.
 XX
 CC The invention relates to methods for inhibiting binding of beta-amyloid
 CC to the p75 nerve growth factor receptor. The methods comprise
 CC contacting the cell with a substance that binds to the p75 nerve growth
 CC factor receptor. The methods are useful in the diagnosis and treatment
 CC of Alzheimer's disease and other neurodegenerative diseases mediated
 CC by beta-amyloid protein, or by aberrant activation of the low affinity
 CC nerve growth factor receptor localised on neural cell surfaces. Such
 CC diseases include autoimmune encephalomyelitis, Huntington's disease,
 CC Pick's disease, corticobasal degeneration, progressive supranuclear
 CC palsy, Gerotman-Straussler Scheinker syndrome, Niemann-Pick disease
 CC and Down's syndrome. The present sequence is a cyclic peptide
 CC comprising a fragment of the human beta-amyloid protein to which a
 CC cysteine residue has been added at each end. The peptide inhibits
 CC binding of beta-amyloid to the p75 nerve growth factor receptor.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 57; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVGSNKGAIK 10
 DB 1 CVGSNKGAIK 10
 RESULT 4
 ABB07973
 ID ABB07973 standard; peptide; 10 AA.
 XX
 AC ABB07973;
 XX
 DT 12-AUG-2002 (first entry)
 XX
 DE Beta-amyloid p75NTR binding inhibiting cyclic peptide.
 XX
 KW Beta-amyloid; p75; nerve growth factor receptor; NGFR; anti-apoptotic;
 KW Alzheimer's disease; neurotrophin receptor; NTR; human; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..10
 FT /note= "disulphide bridge"
 XX
 PN US2002051988-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-MAY-2001; 2001US-0866898.
 XX
 PR 29-SEP-1998; 98US-0163095.
 PR 28-MAR-1996; 96US-0625765.
 PR 28-MAR-1997; 97WO-US04966.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Gilchrist BA, Yaar M;
 XX
 DR WPI; 2002-443695/47.
 XX
 CC Evaluating risk of an individual to develop Alzheimer's disease using
 CC cultured neural crest-derived melanocytes and methods of therapy for
 CC Alzheimer's disease using peptides that bind to the neurotrophin
 CC receptor -
 XX
 PS Claim 4; Page 8; 19pp; English.
 XX
 CC The invention relates to a method of inhibiting beta-amyloid binding to

CC the p75 nerve growth factor receptor (NGFR) of a cell. The method
 CC involves contacting the cell with a substance having the amino acid
 CC sequence lysine-glycine-lysine or lysine-glycine-alanine. The substance
 CC binds to the p75 NGFR resulting in the inhibition of beta-amyloid protein
 CC or beta-amyloid peptide binding to the p75 NGFR. The invention is useful
 CC for evaluating the risk of an individual to develop Alzheimer's disease
 CC and methods of therapy for Alzheimer's disease using peptides that bind
 CC to the neurotrophin receptor (NTR) and competitively inhibit the binding
 CC of beta-amyloid to the receptor. In vitro methods are also provided for
 CC screening substances and identifying those capable of inhibiting, or
 CC decreasing cell apoptosis mediated by beta-amyloid. The present sequence
 CC represents a cyclic peptide that competes for p75NTR binding with
 CC the beta-amyloid peptide.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 57; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CVGSNKGAIK 10
 DB 1 CVGSNKGAIK 10
 RESULT 5
 AAW45343
 ID AAW45343 standard; peptide; 8 AA.
 XX
 AC AAW45343;
 XX
 DT 08-MAY-1998 (first entry)
 XX
 DE Beta-amyloid fragment (residues 24-31).
 XX
 KW Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment;
 KW neurotrophin receptor p75; p75NTR; cyclic.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9737228-A1.
 XX
 PD 09-OCT-1997.
 XX
 PF 28-MAR-1997; 97WO-US04966.
 XX
 PR 29-MAR-1996; 96US-0625765.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 PI Gilchrist BA, Yaar M;
 XX
 DR WPI; 1997-512306/47.
 XX
 CC Evaluating risk of individual to develop Alzheimer's - uses cultured
 CC epidermal melanocyte(s), also useful for developing therapies for
 CC neuro-degenerative diseases
 XX
 PS Disclosure; Page 10; 42pp; English.
 XX
 CC The present sequence represents residues 24 to 31 of beta-amyloid. A
 CC cyclic peptide was synthesised by attaching two cysteine residues to the
 CC beginning and the end of the fragment. The invention relates to a new
 CC method for evaluating the risk of an individual to develop Alzheimer's
 CC disease using cultured neural crest-derived melanocytes. Also
 CC described are methods of therapy for Alzheimer's disease using peptides
 CC (AAW45343-6) that bind to the neurotrophin receptor p75 nerve growth
 CC factor receptor (NGFR) and competitively inhibit the binding of a beta-
 CC amyloid to the p75 NGFR. The methods can be used for diagnosing and
 CC treating Alzheimer's disease and other neurodegenerative diseases
 CC mediated by beta-amyloid protein, or by aberrant activation of the low
 CC affinity NGFR localised on neural cell surfaces, such as autoimmune

CC encephalomyelitis, Huntington's disease, cortico-basal degeneration,
 CC progressive supra-nuclear palsy, Gerotman-Straussler Scheinker syndrome,
 CC Niemann-Pick disease, and progressive supranuclear palsy. In the
 CC diagnostic tests, the human melanocytes, which are easily obtainable
 CC from skin biopsies, are good model cells for the study and diagnosis of
 CC Alzheimer's disease.

XX SQ Sequence 8 AA;

Query Match 68.4%; Score 39; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 | | | | | | | |
 DB 1 VGSNKGAI 8

RESULT 6

AAV39236
 ID AAV39236 standard; peptide; 8 AA.

AC AAV39236;

XX 23-NOV-1999 (first entry)

DE Beta-amyloid fragment for generation of p75NTR inhibiting peptides.

KW p75NTR; p75 neurotrophin receptor; nerve growth factor;
 KW NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid fragment;
 KW Alzheimer's disease; pseudo-ligand; hair growth; hair colour;
 KW skin colour; alopecia areata; male pattern baldness.

XX Synthetic.

PN W09939728-A2.

XX 12-AUG-1999.

XX 03-FEB-1999; 99WO-US02362.

XX 04-FEB-1998; 98US-0018194.

XX (UYBO-) UNIV BOSTON.

XX Eller M, Gilchrest BA, Yaar M;

XX WPI; 1999-539950/45.

XX Controlling or manipulating melanocyte and keratinocyte cell death,
 PT useful for treating, e.g. alopecia areata

XX Disclosure; Page 15; 67pp; English.

XX This sequence is amino acids 24-31 of beta-amyloid. This sequence can be
 CC used to generate cyclic peptide AAV39233. The cyclic peptide competes
 CC with and competitively inhibits beta-amyloid binding to the p75
 CC neurotrophin receptor (p75NTR). p75NTR is a low affinity nerve growth
 CC factor (NGF) receptor which is expressed by melanocytes and keratinocytes
 CC of the basal epidermis. Apoptosis can be inhibited by p75NTR via the
 CC upregulation of the Bcl-2 protein. If the receptor is occupied by
 CC appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other
 CC examples of appropriate ligands include this cyclic peptide. This peptide
 CC is based on the sequence of the binding fragment of beta-amyloid, which
 CC binds to p75NTR in Alzheimer's disease. This cyclic peptide can be used
 CC in methods to control or manipulate keratinocyte or melanocyte cell
 CC death. The methods involve using this peptide or peptides AAV39234-V39235
 CC to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting
 CC apoptosis. The new method can induce or maintain hair growth, hair colour
 CC or skin colour. Inducing or maintaining hair growth is useful for
 CC treating alopecia areata or male pattern baldness in vertebrates.

XX SQ Sequence 8 AA;

Query Match 68.4%; Score 39; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 | | | | | | | |
 DB 1 VGSNKGAI 8

RESULT 7

AAG64001
 ID AAG64001 standard; peptide; 8 AA.

XX AAG64001;

XX 31-AUG-2001 (first entry)

XX Human beta-amyloid peptide.

DE Human; beta-amyloid; 'nootropic; neuroprotective; anticonvulsant;
 KW p75 nerve growth factor receptor; inhibitor; Alzheimer's disease;
 KW neurodegenerative disease.

XX Homo sapiens.

XX US6242416-B1.

XX 05-JUN-2001.

XX 29-SEP-1998; 98US-0163095.

XX 29-MAR-1996; 96US-0625765.

XX 28-MAR-1997; 97WO-US04966.

XX (UYBO-) UNIV BOSTON.

XX Gilchrest BA, Yaar M;

XX WPI; 2001-380482/40.

XX Inhibition of beta-amyloid binding to the p75 nerve growth factor
 PT receptor using polypeptides, useful in the diagnosis and treatment of
 PT e.g. Alzheimer's disease

XX Claim 2; Column 7; 16pp; English.

XX The invention relates to methods for inhibiting binding of beta-amyloid
 CC to the p75 nerve growth factor receptor. The methods comprise
 CC contacting the cell with a substance that binds to the p75 nerve growth
 CC factor receptor. The methods are useful in the diagnosis and treatment
 CC of Alzheimer's disease and other neurodegenerative diseases mediated
 CC by beta-amyloid protein, or by aberrant activation of the low affinity
 CC nerve growth factor receptor localised on neural cell surfaces. Such
 CC diseases include autoimmune encephalomyelitis, Huntington's disease,
 CC Pick's disease, corticobasal degeneration, progressive supranuclear
 CC palsy, Gerotman-Straussler Scheinker syndrome, Niemann-Pick disease
 CC and Down's syndrome. The present sequence is a fragment of the
 CC human beta-amyloid protein. It may be used to produce a cyclic
 CC decapeptide that inhibits binding of beta-amyloid to the p75 nerve
 CC growth factor receptor.

XX SQ Sequence 8 AA;

Query Match 68.4%; Score 39; DB 22; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 | | | | | | | |
 DB 1 VGSNKGAI 8

RESULT 8
 ABB07970
 ID ABB07970 standard; peptide; 8 AA.
 XX AC ABB07970;
 XX DT 12-AUG-2002 (first entry)
 XX DE Beta-amyloid peptide fragment (residues 24-31).
 XX DE Beta-amyloid; p75; nerve growth factor receptor; NGFR; anti-apoptotic;
 KW Alzheimer's disease; neurotrophin receptor; human.
 XX OS Homo sapiens.
 XX PN US2002051988-A1.
 XX PD 02-MAY-2002.
 XX PF 29-MAY-2001; 2001US-0866898.
 XX PR 29-SEP-1998; 98US-0163095.
 XX PR 29-MAR-1996; 96US-0625765.
 XX PR 28-MAR-1997; 97WO-US04966.
 XX PA (UYBO-) UNIV BOSTON.
 XX PI Gilchrist BA, Yaar M;
 XX DR WPI; 2002-443695/A7.
 XX PT Evaluating risk of an individual to develop Alzheimer's disease using
 PT cultured neural crest-derived melanocytes and methods of therapy for
 PT Alzheimer's disease using peptides that bind to the neurotrophin
 PT receptor -
 XX PS Claim 4; Page 4; 19pp; English.
 XX CC The invention relates to a method of inhibiting beta-amyloid binding to
 CC the p75 nerve growth factor receptor (NGFR) of a cell. The method
 CC involves contacting the cell with a substance having the amino acid
 CC sequence lysine-glycine-lysine or lysine-glycine-alanine. The substance
 CC binds to the p75 NGFR resulting in the inhibition of beta-amyloid protein
 CC or beta-amyloid peptide binding to the p75 NGFR. The invention is useful
 CC for evaluating the risk of an individual to develop Alzheimer's disease
 CC and methods of therapy for Alzheimer's disease using peptides that bind
 CC to the neurotrophin receptor and competitively inhibit the binding of
 CC beta-amyloid to the receptor. In vitro methods are also provided for
 CC screening substances and identifying those capable of inhibiting, or
 CC decreasing cell apoptosis mediated by beta-amyloid. The present sequence
 CC represents a beta-amyloid peptide fragment.
 XX SQ Sequence 8 AA;
 Query Match 68.4%; Score 39; DB 23; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;
 QY 2 VGSNKGAI 9
 DB 1 VGSNKGAI 8
 RESULT 9
 AAB46234
 ID AAB46234 standard; peptide; 10 AA.
 XX AC AAB46234;
 XX DT 04-APR-2001 (first entry)
 XX DE Human APP derived immunogenic peptide #30.
 XX PF Human APP derived immunogenic peptide #30.
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 XX amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO200072880-A2.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US14810.
 XX PR 28-MAY-1999; 99US-0322289.
 XX PA (NEUR-) NEURALAB LTD.
 XX PI Schenk DB, Bard F, Vasquez NJ, Yednock T;
 XX DR WPI; 2001-032104/04.
 XX PT Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX PS Disclosure; Figure 19; 143pp; English.
 XX CC This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX SQ Sequence 10 AA;
 Query Match 68.4%; Score 39; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 0;
 QY 2 VGSNKGAI 9
 DB 3 VGSNKGAI 10
 RESULT 10
 AAB46235
 ID AAB46235 standard; peptide; 10 AA.
 XX AC AAB46235;
 XX DT 04-APR-2001 (first entry)
 XX DE Human APP derived immunogenic peptide #31.
 XX PF Human APP derived immunogenic peptide #31.
 KW Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 XX amyloid precursor protein; Alzheimer's disease.
 XX OS Homo sapiens.
 XX PN WO200072880-A2.
 XX PD 07-DEC-2000.
 XX PF 26-MAY-2000; 2000WO-US14810.

PR 28-MAY-1999; 99US-0322289.
 XX (NEUR-) NEURALAB LTD.
 PA Schenk DB, Bard F, Vasquez NJ, Yednock T;
 PI WPI; 2001-032104/04.
 XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX Sequence 10 AA;
 SQ Query Match 68.4%; Score 39; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VGSNKGAI 9
 Db | | | | | | | |
 2 VGSNKGAI 9
 RESULT 11
 AAB46236
 ID AAB46236 standard; peptide; 10 AA.
 AC AAB46236;
 XX 04-APR-2001 (first entry)
 DT Human APP derived immunogenic peptide #32.
 XX Amyloid deposit; APP; Abeta; brain; human; clearing response; neurotropic;
 KW Fc receptor mediated phagocytosis; immunogenic response; neuroprotective;
 KW amyloid precursor protein; Alzheimer's disease.
 XX Homo sapiens.
 OS WO200072880-A2.
 XX 07-DEC-2000.
 PD 26-MAY-2000; 2000WO-US14810.
 PF 28-MAY-1999; 99US-0322289.
 XX (NEUR-) NEURALAB LTD.
 PA Schenk DB, Bard F, Vasquez NJ, Yednock T;
 PI WPI; 2001-032104/04.
 XX Preventing or treating a disease associated with amyloid deposits,
 PT especially Alzheimer's disease, comprises administering amyloid
 PT specific antibody -
 XX

PS Disclosure; Figure 19; 143pp; English.
 XX This invention describes a novel method of preventing or treating a
 CC disease associated with amyloid deposits of amyloid precursor protein
 CC (APP) Abeta fragments in the brain of a patient, which comprises
 CC administering to the patient: (a) an antibody that binds to Abeta, the
 CC antibody binds to an amyloid deposit and induces a clearing response (Fc
 CC receptor mediated phagocytosis) against it (b) a polypeptide containing
 CC an N-terminal segment of at least residues 1-5 of Abeta; or (c) an agent
 CC that induces an immunogenic response against residues 1-3 to 7-11 of
 CC Abeta. The products of the invention have neurotropic and neuroprotective
 CC activity. The method is also useful for monitoring a course of treatment
 CC being administered to a patient e.g. active and passive immunization. The
 CC methods are useful for prophylactic and therapeutic treatment of
 CC Alzheimer's disease.
 XX Sequence 10 AA;
 SQ Query Match 68.4%; Score 39; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VGSNKGAI 9
 Db | | | | | | | |
 1 VGSNKGAI 8
 RESULT 12
 AAU93989
 ID AAU93989 standard; Peptide; 11 AA.
 XX AAU93989;
 AC 02-JUL-2002 (first entry)
 DT Human beta-amyloid B cell epitope #3.
 XX Immunogenic; hepatitis B core protein; hepatitis B core; Hbc;
 KW vaccine; B cell epitope; T cell epitope; immunostimulant.
 XX Homo sapiens.
 OS WO200214478-A2.
 XX 21-FEB-2002.
 PD 16-AUG-2001; 2001WO-US41759.
 PF 16-AUG-2000; 2000US-225843P.
 PR 22-AUG-2000; 2000US-226867P.
 PR 15-AUG-2001; 2001US-0930915.
 XX (APOV-) APOVIA INC.
 PA Birkett AJ;
 PI WPI; 2002-257601/30.
 DR Novel recombinant hepatitis B core protein, termed as chimeric
 PT hepatitis B core protein, displays immunogenic epitopes at N-terminus,
 PT Hbc immunogenic loop with linker for conjugated epitope and C-terminus
 PT -
 XX Disclosure; Page 38; 289pp; English.
 PS The invention relates to a recombinant hepatitis B core protein, termed as chimeric
 CC i.e. a chimeric hepatitis B core (Hbc) protein (I), displaying one or
 CC more immunogenic epitopes at the N-terminus, Hbc immunogenic loop (L) or
 CC C-terminus, or having a heterologous linker for a conjugated epitope in
 CC (L), and containing a Cys residue at, or near, the C-terminus that
 CC confers enhanced stability to the particles. A vaccine comprising (I) is
 CC useful for inducing an immune response in an inoculated host animal, by
 CC inoculating a host animal with the vaccine, and maintaining that

CC inoculated animal for a time period sufficient for that animal to
 CC develop an immune response. The immunogenic particles formed using (I)
 CC are substantially free of binding to nucleic acids, and are most stable
 CC than the particle formed from otherwise identical HBC chimera that lacks
 CC the C-terminal residue or in which a C-terminal Cys is replaced by
 CC another residue. The chimera particles are most stable on storage in
 CC aqueous compositions that are particles of similar sequence that lack any
 CC C-terminal Cys residues. The chimera molecule exhibits the self-assembly
 CC not exhibiting the nucleic acid binding of those native particles, and
 CC excellent B cell and T cell immunogenicities. The chimera particles are
 CC typically prepared in higher yield than similar particles that are free
 CC of a C-terminal Cys. The particles are often far more immunogenic than
 CC the similar conjugates that lack a C-terminal Cys. Immunogenicities of
 CC particles assembled from the chimera molecules are enhanced as compared to
 CC similar particles assembled from chimera molecules lacking at least one
 CC C-terminal Cys. AAU93802-AAU93997 represent immunogenic HBC particles
 CC amino acid sequences and related sequences of the invention.

XX Sequence 11 AA;
 SQ Query Match 68.4%; Score 39; DB 23; Length 11;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 DB 3 VGSNKGAI 10

RESULT 13
 AAB91782
 ID AAB91782 standard; Peptide; 14 AA.

XX AAB91782;

XX 22-JUN-2001 (first entry)

XX Amyloid beta-protein fragment peptide SEQ ID NO:958.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT

XX Disclosure; Page 507; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a

CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX Sequence 14 AA;

QY Query Match 68.4%; Score 39; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. No. 2;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 DB 3 VGSNKGAI 10

RESULT 14
 AAB91788
 ID AAB91788 standard; Peptide; 14 AA.

XX AAB91788;

XX 22-JUN-2001 (first entry)

XX Amyloid beta-protein fragment peptide SEQ ID NO:964.

XX Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.
 OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

XX 17-MAY-2000; 2000WO-US13576.

XX 17-MAY-1999; 99US-0134406.

XX 10-SEP-1999; 99US-0153406.

XX 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 PT peptidase degradation, useful for increasing length of in vivo activity
 PT

XX Disclosure; Page 509; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent

CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX Sequence 14 AA;

Query Match 68.4%; Score 39; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. NO. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 |||||
 Db 3 VGSNKGAI 10

RESULT 15

AAB91815
 ID AAB91815 standard; Peptide; 14 AA.

AC AAB91815;

DT 22-JUN-2001 (first entry)

DE Amyloid beta-protein fragment peptide SEQ ID NO:991.

KW Protection; endogenous therapeutic peptide; peptidase; conjugation;
 KW blood component; modification; succinimidyl; maleimido group; amino;
 KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.

XX Homo sapiens.

OS Synthetic.

XX WO200069900-A2.

XX 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

XX (CONJ-) CONJUCHEM INC.

XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudeau K;

XX WPI; 2001-112059/12.

XX Modifying and attaching therapeutic peptides to albumin prevents
 XX peptidase degradation, useful for increasing length of in vivo activity

XX Disclosure; Page 519; 733pp; English.

XX The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.

CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

SQ Sequence 14 AA;

Query Match 68.4%; Score 39; DB 22; Length 14;
 Best Local Similarity 100.0%; Pred. NO. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 |||||
 Db 3 VGSNKGAI 10

Search completed: November 9, 2002, 14:01:17
 Job time : 34.8462 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:59 ; Search time 13.0769 Seconds
(without alignments)
22.500 Million cell updates/sec

Title: US-09-632-748-4

Perfect score: 57

Sequence: 1 CVGSNKGAIK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	4	US-09-163-095-4
2	39	68.4	8	4	US-09-163-095-1
3	39	68.4	26	1	US-08-304-585-7
4	39	68.4	33	2	US-08-609-090-4
5	39	68.4	34	2	US-08-475-578A-4
6	39	68.4	35	1	US-08-304-585-6
7	39	68.4	35	2	US-08-612-785B-16
8	39	68.4	35	2	US-08-612-785B-36
9	39	68.4	35	2	US-08-612-785B-39
10	39	68.4	35	2	US-08-612-785B-40
11	39	68.4	35	4	US-08-617-267C-16
12	39	68.4	36	2	US-08-609-090-6
13	39	68.4	38	1	US-08-302-808-1
14	39	68.4	38	2	US-07-737-371E-68
15	39	68.4	38	2	US-08-986-948-1
16	39	68.4	38	6	5262332-1
17	39	68.4	39	1	US-08-304-585-5
18	39	68.4	39	1	US-08-302-808-2
19	39	68.4	39	2	US-08-609-090-7
20	39	68.4	39	2	US-08-682-245A-1
21	39	68.4	39	2	US-08-986-948-2
22	39	68.4	40	1	US-07-744-767A-1
23	39	68.4	40	1	US-08-235-400-2
24	39	68.4	40	1	US-08-476-464A-2
25	39	68.4	40	1	US-08-304-585-1
26	39	68.4	40	1	US-08-304-585-8
27	39	68.4	40	1	US-08-302-808-3

28 39 68.4 40 2 US-08-433-734-1 Sequence 1, Appli
29 39 68.4 40 2 US-08-609-090-8 Sequence 8, Appli
30 39 68.4 40 2 US-07-737-371E-69 Sequence 69, Appli
31 39 68.4 40 2 US-08-682-245A-2 Sequence 2, Appli
32 39 68.4 40 2 US-08-986-948-3 Sequence 3, Appli
33 39 68.4 40 2 US-08-461-216-1 Sequence 1, Appli
34 39 68.4 40 4 US-08-959-148-1 Sequence 1, Appli
35 39 68.4 40 4 US-09-242-724-22 Sequence 22, Appli
36 39 68.4 40 4 US-08-723-661B-1 Sequence 1, Appli
37 39 68.4 40 4 US-09-062-365-3 Sequence 3, Appli
38 39 68.4 40 5 PCT-US92-06700-1 Sequence 1, Appli
39 39 68.4 41 1 US-07-819-361-1 Sequence 1, Appli
40 39 68.4 41 1 US-08-302-808-4 Sequence 4, Appli
41 39 68.4 41 2 US-08-682-245A-3 Sequence 3, Appli
42 39 68.4 41 2 US-08-986-948-4 Sequence 4, Appli
43 39 68.4 42 1 US-07-744-767A-2 Sequence 2, Appli
44 39 68.4 42 1 US-08-179-574-1 Sequence 1, Appli
45 39 68.4 42 1 US-08-271-162-5 Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-163-095-4
; Sequence 4, Application US/09163095
; Patent No. 6242416
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; TITLE OF INVENTION: ALZHEIMER'S DISEASE
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/163,095
; CURRENT FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: PCT/US97/04966
; EARLIER FILING DATE: 1997-03-28
; EARLIER APPLICATION NUMBER: 08/625,765
; EARLIER FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
US-09-163-095-4

Query Match 100.0%; Score 57; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0011;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVGSNKGAIK 10

Db 1 CVGSNKGAIK 10

RESULT 2
US-09-163-095-1
; Sequence 1, Application US/09163095
; Patent No. 6242416
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; TITLE OF INVENTION: ALZHEIMER'S DISEASE
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/163,095
; CURRENT FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: PCT/US97/04966
; EARLIER FILING DATE: 1997-03-28
; EARLIER APPLICATION NUMBER: 08/625,765

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; EARLIER FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PPT
; ORGANISM: Homo sapiens
US-09-163-095-1

Query Match      68.4%; Score 39; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
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Db 1 VGSNKGAI 8

RESULT 3
US-08-304-585-7
; Sequence 7, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; APPLICANT: Mantyh, Patrick W.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 26 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-304-585-7

Query Match      68.4%; Score 39; DB 1; Length 26;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
   |||||
Db 15 VGSNKGAI 22

RESULT 4
US-08-609-090-4
; Sequence 4, Application US/08609090
; Patent No. 5840838
; GENERAL INFORMATION:
; APPLICANT: HENSLEY, Kenneth
; APPLICANT: BUTTERFIELD, D. A.
; APPLICANT: CARNEY, John M.
; APPLICANT: AKSENOV, Michael
; TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
; TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE PRICE LEBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,090
; FILING DATE: 29-FEB-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Kraus, Eric J.
; REGISTRATION NUMBER: 36,190
; REFERENCE/DOCKET NUMBER: 434-059
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; TELEFAX: 703-684-1124
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-609-090-4

Query Match      68.4%; Score 39; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
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Db 24 VGSNKGAI 31

RESULT 5
US-08-475-579A-4
; Sequence 4, Application US/08475579A
; Patent No. 5854215
; GENERAL INFORMATION:
; APPLICANT: Mark A. Findeis et al.
; TITLE OF INVENTION: Modulators of {SYMBOL 98 \f "Symbol"}-Amyloid Peptide Aggre
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,579A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,831
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: PPI-002CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-475-579A-4

Query Match 68.4%; Score 39; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 18 VGSNKGAI 25

RESULT 6
US-08-304-585-6
; Sequence 6, Application US/08304585
; Patent No. 5721106
; GENERAL INFORMATION:
; APPLICANT: Maggio, John E.
; TITLE OF INVENTION: LABELLED BETA-AMYLOID PEPTIDE AND
; TITLE OF INVENTION: METHODS FOR USE IN DETECTING ALZHEIMER'S DISEASE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Muetting, Raasch, Gebhardt & Schwappach, P.A.
; STREET: P.O. Box 581415
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55458-1415
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/304,585
; FILING DATE: 12-SEP-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Muetting, Ann M.
; REGISTRATION NUMBER: 33,977
; REFERENCE/DOCKET NUMBER: 110.00010120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-305-1217
; TELEFAX: 612-305-1228
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-304-585-6

Query Match 68.4%; Score 39; DB 1; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3;

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/404,831
; FILING DATE: 14-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: P41,106
; REFERENCE/DOCKET NUMBER: PPI-002CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; US-08-475-579A-4

Query Match 68.4%; Score 39; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 19 VGSNKGAI 26

RESULT 8
US-08-612-785B-36
; Sequence 36, Application US/08612785B
; Patent No. 5854204
; GENERAL INFORMATION:
; APPLICANT: Findeis, Mark A. et al.
; TITLE OF INVENTION: AD Peptides that Modulate b-Amyloid
```

Query Match 68.4%; Score 39; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. NO. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels

RESULT 10

Query Match 68.4%; Score 39; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street, Suite 510
CITY: Boston

US-08-612-785B-39
; Sequence 39, Application US/08612785B
; Patent No. 5854204

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/612,785B
 FILING DATE: Herewith
 CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995

FILING DATE: 07-JUN-1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: USSN 08/548,998
 FILING DATE: 27-OCT-1995
 ATTORNEY/AGENT INFORMATION:

NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP3
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-612-785B-40

Query Match 68.4%; Score 39; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 19 VGSNKGAI 26

RESULT 11
US-08-617-267C-16
Sequence 16, Application US/08617267C
Patent No. 6319498
GENERAL INFORMATION:
APPLICANT: Findels, Mark A. et al.
TITLE OF INVENTION: Modulators of Amyloid Aggregation
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD, LLP
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/617,267C
FILING DATE: 14-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/404,831
FILING DATE: 14-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/475,579
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA: USSN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 35 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-617-267C-16

Query Match 68.4%; Score 39; DB 4; Length 35;

Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 19 VGSNKGAI 26

RESULT 12
US-08-609-090-6
Sequence 6, Application US/08609090
Patent No. 5840838
GENERAL INFORMATION:
APPLICANT: HENSLEY, Kenneth
APPLICANT: BUTTERFIELD, D. A.
APPLICANT: CARNEY, John M.
APPLICANT: AKSENOV, Michael
TITLE OF INVENTION: A PROCESS FOR ENHANCING THE ACTIVITY OF
TITLE OF INVENTION: AN OLIGOPEPTIDE OR POLYPEPTIDES
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE PRICE LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,090
FILING DATE: 29-FEB-1996
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kraus, Eric J.
REGISTRATION NUMBER: 36,190
REFERENCE/DOCKET NUMBER: 434-059
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-684-1111
TELEFAX: 703-684-1124
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-609-090-6

Query Match 68.4%; Score 39; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

RESULT 13
US-08-302-808-1
Sequence 1, Application US/08302808
Patent No. 5750349
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5750349uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
TITLE OF INVENTION: DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:

ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/302,808
FILING DATE: 15-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993
FILING DATE: 16-NOV-1993
APPLICATION NUMBER: 334773/1993
FILING DATE: 28-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: DAVID, RESNICK S
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 44631
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-302-808-1

Query Match 68.4%; Score 39; DB 1; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

RESULT 14
US-07-737-371E-68
Sequence 68, Application US/07737371E
Patent No. 5876948
GENERAL INFORMATION:
APPLICANT: Yankner, Bruce A.
TITLE OF INVENTION: SCREENING METHODS TO IDENTIFY
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/737,371E
FILING DATE: 29-JUL-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/559,172
FILING DATE: 27-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 00108/028002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-737-371E-68

Query Match 68.4%; Score 39; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

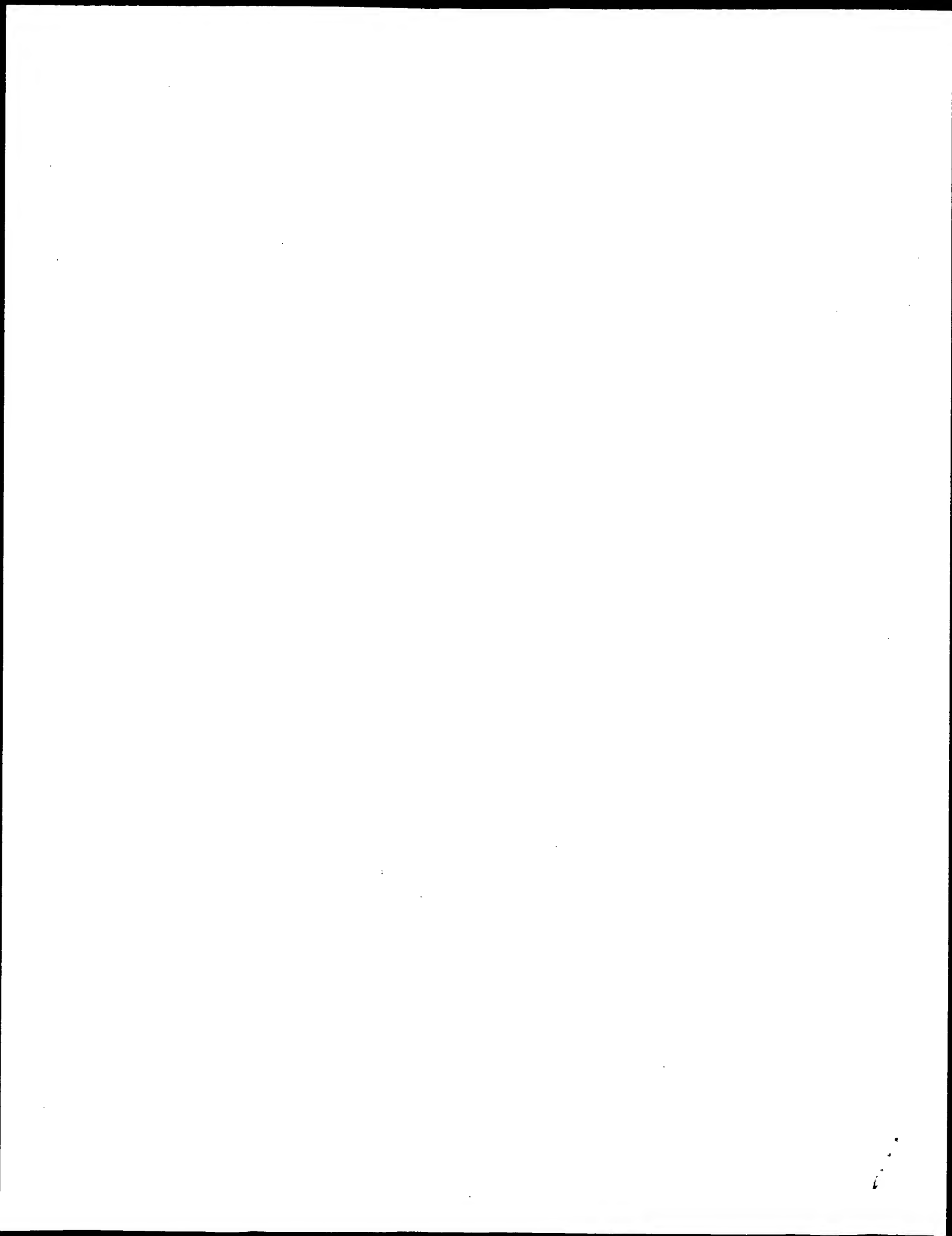
RESULT 15
US-08-986-948-1
Sequence 1, Application US/08986948
Patent No. 5955317
GENERAL INFORMATION:
APPLICANT: SUZUKI, No. 5955317uhiro
APPLICANT: ODAKA, Asano
APPLICANT: KITADA, Chieko
TITLE OF INVENTION: ANTIBODIES TO B-AMYLOIDS OR THEIR
DERIVATIVES AND USE THEREOF
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02019
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/986,948
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/302,808
FILING DATE: 15-SEP-1994
APPLICATION NUMBER: PCT/JP94/00089
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 010132/1993
FILING DATE: 25-JAN-1993
APPLICATION NUMBER: 019035/1993
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 286985/1993

; FILING DATE: 16-NOV-1993
; APPLICATION NUMBER: 334773/1993
; FILING DATE: 28-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 44631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; US-08-986-948-1

Query Match 68.4%; Score 39; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 3.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VGSNKGAI 9
| | | | | | |
Db 24 VGSNKGAI 31

Search completed: November 9, 2002, 14:04:22
Job time : 14.0769 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:56:34 ; Search time 33.8462 Seconds
(without alignments)
39.370 Million cell updates/sec

Title: US-09-632-748-9
Perfect score: 57
Sequence: 1 CATDIKGAEC 10

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	57	100.0	10	AAV39234	Cyclic peptide use
2	40	70.2	311	AA151727	Human secreted pro
3	38	66.7	181	AAU49201	Propionibacterium
4	38	66.7	420	ABG25236	Novel human diagno
5	38	66.7	2703	ABB60266	Drosophila melanog
6	35.5	62.3	554	ABG28140	Novel human diagno
7	35	61.4	56	ABP04269	Human ORFX protein
8	35	61.4	704	AA131165	Amino acid sequenc
9	35	61.4	766	ABG67145	Drosophila melanog
10	35	61.4	977	AA131164	Amino acid sequenc

11	35	61.4	1124	15	AA45440	Human orphan recep
12	35	61.4	1124	16	AA73953	Human TEK tyrosine
13	35	61.4	1124	20	AAV30318	Amino acid sequenc
14	35	61.4	1124	22	AA65945	Amino acid sequenc
15	35	61.4	1124	23	AB95463	Human angiotensin
16	35	61.4	1124	23	AAU78550	Human Tie2 recepto
17	35	61.4	1124	23	AB84857	Human PRO734 prote
18	34.5	60.5	1296	20	AA88448	Caenorhabditis ele
19	34	59.6	9	16	AA83764	NGF derived struct
20	34	59.6	10	16	AA83761	NGF derived struct
21	34	59.6	11	10	AA90623	Peptide to induce
22	34	59.6	11	22	AA64913	Murine nerve growt
23	34	59.6	11	22	AA64915	Rat nerve growth f
24	34	59.6	11	22	AA64917	Human nerve growth
25	34	59.6	12	14	AA41747	Conserved NGF regi
26	34	59.6	12	14	AA41748	Conserved NGF regi
27	34	59.6	13	11	AA07158	Nerve growth facto
28	34	59.6	14	11	AA07161	Synthetic Nerve gr
29	34	59.6	24	12	AA13389	(23-47)hNGF. Synt
30	34	59.6	27	12	AA13393	(9-36)hNGF. Synt
31	34	59.6	27	12	AA13394	(36-62)hNGF. Synt
32	34	59.6	55	23	ABP10396	Human ORFX protein
33	34	59.6	78	12	AA15045	Beta lactamase sig
34	34	59.6	118	10	AA91034	Human nerve growth
35	34	59.6	118	13	AA21874	Chimeric neurotrop
36	34	59.6	118	13	AA29493	NGF, mouse. Mus m
37	34	59.6	119	5	AA40040	Sequence encoded b
38	34	59.6	119	10	AA90133	Human nerve growth
39	34	59.6	119	12	AA13064	Human NGF HindIII-
40	34	59.6	119	12	AA13472	Variant human beta
41	34	59.6	119	16	AA87420	Nerve growth facto
42	34	59.6	119	21	AA80347	Human beta-nerve g
43	34	59.6	120	13	AA21863	Chimeric neurotrop
44	34	59.6	120	13	AA21864	Chimeric neurotrop
45	34	59.6	120	13	AA21867	Chimeric neurotrop

ALIGNMENTS

RESULT 1

AAV39234
ID AAV39234 standard; peptide; 10 AA.

AC AAV39234;

DT 23-NOV-1999 (first entry)

XX Cyclic peptide used to inhibit p75NTR mediated apoptosis.

XX Cyclic peptide; p75NTR; p75 neurotrophin receptor; nerve growth factor;

KW NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid;

KW Alzheimer's disease; pseudo-ligand; hair growth; hair colour;

KW skin colour; alopecia areata; male pattern baldness.

OS Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1

FT FT /note= "N-terminus is attached via a peptide bond to the C-terminus amino acid at position 10"

FT FT /note= "C-terminus is attached via a peptide bond to the N-terminus amino acid at position 1"

FT FT

PN WO9939728-A2.

PD 12-AUG-1999.

XX 03-FEB-1999; 99WO-US2362.

PR 04-FEB-1998; 98US-0018194.

XX

PA (UYBO-) UNIV BOSTON.
 XX
 PI Eller M, Gilchrist BA, Yaar M;
 XX
 DR WPI; 1999-539950/45.
 XX
 PT Controlling or manipulating melanocyte and keratinocyte cell death,
 PT useful for treating, e.g. alopecia areata
 XX
 PS Claim 4; Page 40; 67pp; English.
 XX
 CC This sequence is a cyclic peptide which competes with and competitively
 CC inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR).
 CC p75NTR is a low affinity nerve growth factor (NGF) receptor which is
 CC expressed by melanocytes and keratinocytes of the basal epidermis.
 CC Apoptosis can be inhibited by p75NTR via the upregulation of the Bcl-2
 CC protein. If the receptor is occupied by appropriate ligands e.g.
 CC neurotrophins, apoptosis is inhibited. Other examples of appropriate
 CC ligands include this cyclic peptide. This peptide is based on the
 CC sequence of the binding fragment of beta-amyloid, which binds to
 CC p75NTR in Alzheimer's disease. This cyclic peptide can be used in
 CC methods to control or manipulate keratinocyte or melanocyte cell death.
 CC The methods involve using this peptide or peptides AAY39233/X39235 to
 CC bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting
 CC apoptosis. The new method can induce or maintain hair growth, hair colour
 CC or skin colour. Inducing or maintaining hair growth is useful for
 CC treating alopecia areata or male pattern baldness in vertebrates.
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 57; DB 20; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CATDIKGAEC 10
 Db | | | | | | | |
 1 CATDIKGAEC 10
 RESULT 2
 AAB51727
 ID AAB51727 standard; Protein; 311 AA.
 XX
 AC AAB51727;
 XX
 DT 16-FEB-2001 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 3.
 XX
 KW Human; secreted protein; immunosuppressive; antiarthritic; antirheumatic;
 KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
 KW neurotropic; neuroprotective; antibacterial; virucide; fungicide;
 KW ophthalmological; vulnary; autoimmune disease; rheumatoid arthritis;
 KW hyperproliferative disorders; cancer; cardiovascular disorder;
 KW cardiac arrest; cerebrovascular disorder; nervous system disorder;
 KW Alzheimer's disease; ocular disorder; wound healing; skin aging.
 XX
 OS Homo sapiens.
 XX
 PN WO2000061625-A1.
 XX
 PD 19-OCT-2000.
 XX
 PF 06-APR-2000; 2000WO-US08981.
 XX
 PR 09-APR-1999; 99US-0128701.
 PR 20-JAN-2000; 2000US-0177166.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX

DR WPI; 2000-619226/59.
 XX
 PT New nucleic acid molecules encoding 48 human secreted proteins for
 PT diagnosing, preventing, treating or ameliorating medical conditions and
 PT used as food additives or preservatives -
 XX
 PS Disclosure; Page 446; 500pp; English.
 XX
 CC Polynucleotide sequences AAC93422 - AAC93449 represent cDNA encoding
 CC human secreted proteins AAB51724 - AAB51777. Sequences AAB51778 -
 CC AAB51825 represent alternative polypeptides encoded by the genes, and
 CC amino acid sequences to which they are homologous. The genes and proteins
 CC have activities dependent on the tissues and cells in which they are
 CC expressed. Examples of their activities include immunosuppressive;
 CC antihypertic; antirheumatic; antiproliferative; cytostatic; cardiant;
 CC vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial;
 CC virucide; fungicide; ophthalmological; and vulnerary. The secreted
 CC proteins, polynucleotides, antagonists and agonists may be useful in
 CC treating, preventing and/or diagnosing diseases and disorders such as
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,
 CC infections caused by bacteria, viruses and fungi and ocular disorders
 CC e.g. corneal infection. The polypeptides can also be used to aid wound
 CC healing and epithelial cell proliferation, to prevent skin aging due to
 CC sunburn, to maintain organs before transplantation, for supporting cell
 CC culture of primary tissues, to regenerate tissues and in chemotaxis. The
 CC polypeptides can also be used as a food additive or preservative to
 CC increase or decrease storage capabilities, fat content, lipid, protein,
 CC carbohydrate, vitamins, minerals, cofactors and other nutritional
 CC components. Oligonucleotide AAC93413 - AAC93421 and peptide AAB51723 are
 CC used in the isolation and characterisation of the proteins and
 CC polynucleotides of the invention.
 XX
 SQ Sequence 311 AA;
 Query Match 70.2%; Score 40; DB 21; Length 311;
 Best Local Similarity 50.0%; Pred. No. 60;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CATDIKGAEC 10
 Db | | | | | | | |
 252 CSTDVRGQHC 261
 RESULT 3
 AAU49201
 ID AAU49201 standard; Protein; 181 AA.
 XX
 AC AAU49201;
 XX
 DT 27-FEB-2002 (first entry)
 XX
 DE Propionibacterium acnes immunogenic protein #10097.
 XX
 KW SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;
 KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;
 KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;
 KW dermatological; osteopathic; neuroprotectant.
 XX
 OS Propionibacterium acnes.
 XX
 PN WO200181581-A2.
 XX
 PD 01-NOV-2001.
 XX
 PF 20-APR-2001; 2001WO-US12865.
 XX
 PR 21-APR-2000; 2000US-199047P.
 PR 02-JUN-2000; 2000US-208841P.
 PR 07-JUL-2000; 2000US-216747P.
 XX

DR N-PSDB; ABL04369.
 XX New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 XX
 PS Disclosure; SEQ ID NO 7590; Zipp + Sequence Listing; English.
 XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL01840-ABL16175) and the encoded proteins
 CC (ABR57737-ABR72072).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 2703 AA;
 Query Match 66.7%; Score 38; DB 22; Length 2703;
 Best Local Similarity 60.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
 ||| |||
 Db 437 CATGKGKVD 446

RESULT 6
 ABG28140
 ID ABG28140 standard; Protein; 554 AA.

XX
 AC ABG28140;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #28131.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX
 PD 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

DR N-PSDB; AAS92327.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

XX Claim 20; SEQ ID No 58499; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX
 SQ Sequence 554 AA;

Query Match 62.3%; Score 35.5; DB 22; Length 554;
 Best Local Similarity 70.0%; Pred. No. 6.1e+02;
 Matches 7; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 CATDIKGAEC 10
 || :|||
 Db 102 CA-ELKGAEC 110

RESULT 7
 ABP04269
 ID ABP04269 standard; Protein; 56 AA.

XX
 AC ABP04269;

XX
 DT 24-JUN-2002 (first entry)

XX Human ORFX protein sequence; SEQ ID NO:8520.

XX Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis;
 KW hyperproliferative disorder; psoriasis; benign tumour; haemorrhage;
 KW degenerative disorder; osteoarthritis; neurodegenerative disorder;
 KW cardiovascular disease; diabetes mellitus; systemic lupus erythematosus;
 KW hypertension; hypothyroidism; cholesterol ester storage disease;
 KW immune deficiency; immune disorder; infectious disease;
 KW autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis;
 KW myasthenia gravis.

XX Homo sapiens.

XX WO200192523-A2.

XX 06-DEC-2001.

XX 29-MAY-2001; 2001WO-US10836.

XX 30-MAY-2000; 2000US-206132P.

XX 29-AUG-2000; 2000US-228716P.

XX (CURA-) CURAGEN CORP.

XX Shimkets RA, Leach MD;

XX WPI; 2002-106308/14.

DR N-PSDB; ABN20021.

XX Novel human polypeptides and polynucleotides useful for diagnosing,
 PT preventing and treating cardiovascular disease, neurodegenerative,
 PT hyperproliferative disorders and autoimmune disorders -
 XX Disclosure; SEQ ID 8520; 1037pp; English.

XX The present invention describes substantially purified human proteins

CC (referred to as open reading frame, ORFX, where X is 1-11491 (see Table 1
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
 CC treating or preventing a pathology associated with an ORFX-associated
 CC disorder in humans, and in the manufacture of a medicament for treating a
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide
 CC sequences can be used in gene therapy. ORFX sequences can be used in the
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,
 CC psoriasis, benign tumours, keloid, degenerative disorders, haemorrhage,
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester
 CC storage disease, various immune deficiencies and disorders, infectious
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,
 CC bone degenerative disorders, or periodontal disease, and for gut
 CC protection or regeneration and treatment of lung or liver fibrosis,
 CC reperfusion injury in various tissues and conditions resulting from
 CC systemic cytokine damage.
 CC N.B. The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 56 AA;

Query Match 61.4%; Score 35; DB 23; Length 56;
 Best Local Similarity 55.6%; Pred. No. 79;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGAEC 10

Db :||: ||:|

14 STDVHGAC 22

RESULT 8

ABR31165

ID AAB31165 standard; protein; 704 AA.

AC AAB31165;

DT 02-APR-2001 (first entry)

DE Amino acid sequence of a Tek/Fc fusion protein.

KW Fusion protein; receptor tyrosine kinase; Tek; Fc portion;
 KW immunoglobulin G1; IgG1; angiogenesis; tumour; ocular neovascularisation;
 KW inflammatory disease; arthritis; rheumatism; psoriasis; eye disorder;
 KW diabetic retinopathy; retinopathy; neovascular glaucoma; retinoblastoma;
 KW retrolental fibroplasia; rubeosis; uveitis; macular degeneration;
 KW graft neovascularisation; cancer; metastatic sarcoma; carcinoma;
 KW wound granulation.

XX Synthetic.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 1..18

FT /note= "signal peptide"

FT Protein 19..472

FT /note= "Tek extracellular domain fragment"

FT Protein 473..704

FT /note= "Fc portion"

XX WO200075323-A1.

PN 14-DEC-2000.

XX 07-JUN-2000; 2000WO-US15706.

PF 07-JUN-1999; 95US-0137889.

XX

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XX

XX

XX

XX

XX

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PA (IMMV) IMMUNEX CORP.

XX Cerretti DP, Borges LG, Fanslow WC;

PI WPI; 2001-112149/12.

XX

DR

XX

PT New Tek polypeptides antagonist having a fragment of the Tek

PT extracellular domain, useful for treating mammals with a disease

PT mediated by angiogenesis, e.g. tumors, ocular neovascularisation or

PT inflammatory diseases

XX

PS Claim 17; Page 37-39; 43pp; English.

XX

CC The present sequence represents a fusion protein comprising the

CC extracellular domain of the human receptor tyrosine kinase Tek and the

CC Fc portion of human immunoglobulin (Ig) G1. The Tek fragment lacks all

CC or part of the region containing fibronectin type III (FNIII) motifs, and

CC retains the ability to bind at least one Tek ligand. The fusion

CC polypeptide is an angiogenesis inhibitor, and a Tek antagonist. The

CC polypeptide or soluble Tek multimer, antibodies or antibody fragments are

CC useful for treating a mammal having a disease or condition characterized by

CC angiogenesis, e.g. a solid tumour a condition or disease characterized by

CC ocular neovascularisation. In particular, the Tek antagonists are useful

CC for treating or preventing inflammatory diseases (e.g. arthritis,

CC rheumatism or psoriasis), certain eye disorders (e.g. diabetic

CC retinopathy, retinopathy of prematurity, neovascular glaucoma,

CC retinoblastoma, retrolental fibroplasia, rubeosis, uveitis, macular

CC degeneration or graft neovascularisation), cancer (e.g. metastatic

CC sarcomas or carcinomas), or wound granulation.

XX Sequence 704 AA;

SQ

Query Match 61.4%; Score 35; DB 22; Length 704;

Best Local Similarity 60.0%; Pred. No. 9.3e+02;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

Db :||: ||:|

289 CATGWKGLQC 298

RESULT 9

ABB67145

ID ABB67145 standard; Protein; 766 AA.

AC ABB67145;

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 28227.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;

KW pharmaceutical.

XX

OS Drosophila melanogaster.

XX

PN WO200171042-A2.

XX

PD 27-SEP-2001.

XX

PF 23-MAR-2001; 2001WO-US09231.

XX

PR 23-MAR-2000; 2000US-191637P.

XX

PR 11-JUL-2000; 2000US-0614150.

XX

XX (PEKE) PE CORP NY.

PA

XX

PI Venter JC, Adams M, Li PWD, Myers EW;

XX

XX WPI; 2001-656860/75.

DR N-PSDB; ABL11248.

XX

XX New isolated nucleic acid detection reagent for detecting 1000 or more

PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS Disclosure; SEQ ID NO 28227; 21pp + Sequence Listing; English.

XX
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABU16176-ABU160511), expressed DNA
 CC sequences (ABU161840-ABU16175) and the encoded proteins
 CC (ABU57737-ABU72072).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 766 AA;

Query Match 61.4%; Score 35; DB 22; Length 766;

Best Local Similarity 55.6%; Pred. NO. 1e+03;

Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 9

| | | | |

Db 463 CLTDVQGE 471

RESULT 10

AAB31164

ID AAB31164 standard; protein; 977 AA.

XX

AC AAB31164;

DT 02-APR-2001 (first entry)

XX

DE Amino acid sequence of a Tek/Fc fusion protein.

XX

KW Fusion protein; receptor tyrosine kinase; Tek; Fc portion;
 KW immunoglobulin G1; IgG1; angiogenesis; tumour; ocular neovascularisation;
 KW inflammatory disease; arthritis; rheumatism; psoriasis; eye disorder;
 KW diabetic retinopathy; retinopathy; neovascular glaucoma; retinoblastoma;
 KW retrolental fibroplasia; rubeosis; uveitis; macular degeneration;
 KW graft neovascularisation; cancer; metastatic sarcoma; carcinoma;
 KW wound granulation.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1..18

FT /note= "signal peptide"

FT Protein 19..745

FT /note= "Tek extracellular domain"

FT Protein 746..977

FT /note= "Fc portion"

XX

PN WO200075323-A1.

XX

PD 14-DEC-2000.

XX

XX 07-JUN-2000; 2000WO-US15706.

PF

PR 07-JUN-1999; 99US-0137889.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Cerretti DP, Borges LG, Fanslow WC;

XX

XX WPI; 2001-112149/12.

XX

PT New Tek polypeptides antagonist having a fragment of the Tek
 PT extracellular domain, useful for treating mammals with a disease

PT mediated by angiogenesis, e.g. tumors, ocular neovascularisation or
 PT inflammatory diseases -

PS Claim 41; Page 34-37; 43pp; English.

XX
 CC The present sequence represents a fusion protein comprising the
 CC extracellular domain of the human receptor tyrosine kinase Tek and the
 CC Fc portion of human immunoglobulin (Ig) G1. The Tek fragment lacks all
 CC or part of the region containing fibronectin type III (FNIII) motifs, and
 CC retains the ability to bind at least one Tek ligand. The fusion
 CC polypeptide is an angiogenesis inhibitor, and a Tek antagonist. The
 CC polypeptide or soluble Tek multimer, antibodies or antibody fragments are
 CC useful for treating a mammal having a disease or condition mediated by
 CC angiogenesis, e.g. a solid tumour a condition or disease characterized by
 CC ocular neovascularisation. In particular, the Tek antagonists are useful
 CC for treating or preventing inflammatory diseases (e.g. arthritis,
 CC rheumatism or psoriasis), certain eye disorders (e.g. diabetic
 CC retinopathy, retinopathy of prematurity, neovascular glaucoma,
 CC retinoblastoma, retrolental fibroplasia, rubeosis, uveitis, macular
 CC degeneration or graft neovascularisation), cancer (e.g. metastatic
 CC sarcomas or carcinomas), or wound granulation.

SQ Sequence 977 AA;

Query Match 61.4%; Score 35; DB 22; Length 977;

Best Local Similarity 60.0%; Pred. NO. 1.3e+03;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

| | | | |

Db 289 CATGWKGLQC 298

RESULT 11

AAR45440

ID AAR45440 standard; Protein; 1124 AA.

XX

AC AAR45440;

XX

XX 25-JUN-1994 (first entry)

DT

XX Human orphan receptor kinase.

DE

XX Ork; ligands; antibodies; PCR; amplification.

KW

XX Homo sapiens.

OS

XX Key Location/Qualifiers

FT Peptide 1..18

FT /note= "signal peptide"

FT Region 746..772

FT /note= "transmembrane region"

FT Region 211..340

FT /note= "EGF-like repeat"

FT Misc-difference 44

FT /note= "Cys of immunoglobulin domain"

FT Misc-difference 102

FT /note= "Cys of immunoglobulin domain"

FT Misc-difference 19..1124

FT /note= "claimed fragment"

FT Misc-difference 19..745

FT /note= "claimed fragment"

XX

XX WO9400469-A.

XX

XX 06-JAN-1994.

XX

XX 25-JUN-1993; 93WO-US06093.

XX

XX 26-JUN-1992; 92US-0505600.

XX

XX (IMMV) IMMUNEX CORP.

XX

PI Ziegler SF;
 DR WPI; 1994-026132/03.
 DR N-PSDB; AAQ55179.
 XX
 PT DNA and protein sequences for orphan receptor tyrosine kinase -
 PT and expression vectors for prodn. of recombinant protein and
 PT antibodies specific for the protein, useful in research
 XX
 PS Claim 13; Fig 1; 57pp; English.
 CC Degenerate oligonucleotide primers based on the sequence conserved
 CC in the kinase domain of all receptor tyrosine kinases was used for
 CC PCR of single stranded cDNA from human placental polyA mRNA. PCR
 CC prod. HPK-6 contained a novel sequence which was used as a probe to
 CC isolate longer fragments from a human placental cDNA library. One
 CC clone contained the entire coding region and was called the ork gene.
 CC The gene prod. shown can be used as a research tool in in vitro assays
 CC for detection of ork, its ligands or their interactions.
 CC See also AAR45441.
 XX
 SQ Sequence 1124 AA;
 Query Match 61.4%; Score 35; DB 15; Length 1124;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATDIKGAEC 10
 ||| || :|
 Db 289 CATGWKGLQC 298
 RESULT 12
 AAR73953
 ID AAR73953 standard; Protein; 1124 AA.
 AC AAR73953;
 XX
 DT 22-JAN-1996 (first entry)
 DE Human TEK tyrosine kinase protein.
 XX tie-2; receptor-tyrosine kinase; DNA primer; cancer; angiogenesis;
 KW vasculogenesis; tek.
 XX Homo sapiens.
 OS WO9513387-A1.
 PN 18-MAY-1995.
 PD
 XX 12-NOV-1994; 94WO-EP03767.
 PF 12-NOV-1993; 93US-0152552.
 PR (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
 PA
 XX Risau W;
 PI WPI; 1995-194105/25.
 DR
 XX New tie-2 receptor tyrosine kinase and related nucleic acid - and
 PT methods for detecting tie-2 modulators for treating eg cancer,
 PT associated with angiogenesis and vasculogenesis
 XX Disclosure; Page 49; 81pp; English.
 PS
 CC This protein is the human homolog of mouse tie-2 receptor
 CC tyrosine kinase.
 XX
 SQ Sequence 1124 AA;
 Query Match 61.4%; Score 35; DB 16; Length 1124;

Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATDIKGAEC 10
 ||| || :|
 Db 289 CATGWKGLQC 298
 RESULT 13
 AAY30318
 ID AAY30318 standard; protein; 1124 AA.
 XX
 AC AAY30318;
 XX
 DT 15-NOV-1999 (first entry)
 DE Amino acid sequence of TEK (also known as TIE2) protein.
 XX TEK protein; TIE2 protein; receptor tyrosine kinase; T cell response;
 KW immune response; endothelial cell; tumor-associated vasculature;
 KW coagulation; thrombosis; cancer; anticancer vaccine.
 XX Homo sapiens.
 OS WO9943801-A1.
 PN 02-SEP-1999.
 PD 26-FEB-1999; 99WO-GB00583.
 PF 26-FEB-1998; 98GB-0004121.
 PR (CANC-) CANCER RES CAMPAIGN TECHNOLOGY.
 PA Durrant LG, Hewett PW, Ramage JM, Spendlove I;
 PI WPI; 1999-540586/45.
 DR
 XX New peptides containing at least one epitope from Tek receptor
 PT tyrosine kinase, used in vaccines against cancer
 XX Disclosure; Fig 1; 56pp; English.
 PS
 CC The present sequence represents the TEK protein, also known as TIE2
 CC protein. TEK is a receptor tyrosine kinase. TEK contains epitopes
 CC which bind to MHC. The presentation of TEK epitopes can also stimulate
 CC helper cell and/or cytotoxic T cell responses. The immune response is
 CC directed against endothelial cells in the tumor-associated
 CC vasculature and includes production of antibodies that bind to the
 CC cells, causing coagulation and thrombosis. The immune response is
 CC targeted to endothelial cells lining blood vessels of the tumor (these
 CC cells overexpress Tek), so damage to even a few cells will kill many
 CC tumor cells. These target cells are accessible to the immune response
 CC and problems of antigenic heterogeneity, MHC loss and resistance to
 CC apoptosis (associated with epithelial cells) are unlikely to occur in
 CC normal endothelial cells. TEK epitopes (see AAY30320-24) are used to
 CC generate antibodies, and for prevention and treatment of cancer.
 CC The peptides, and recombinant DNA constructs or viral vectors that
 CC express them, are useful as anticancer vaccines to target endothelial
 CC cells that line blood vessels of the tumor.
 XX
 SQ Sequence 1124 AA;
 Query Match 61.4%; Score 35; DB 20; Length 1124;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATDIKGAEC 10
 ||| || :|
 Db 289 CATGWKGLQC 298
 RESULT 14

AAG65945
 ID AAG65945 standard; protein; 1124 AA.
 AC AAG65945;
 XX
 DT 11-FEB-2002 (first entry)
 XX
 DE Amino acid sequence of human Tie-2.
 KW Tie-2; catalytic domain; receptor tyrosine kinase; crystalline; human;
 KW cytosolic; vasotropic; antineuritic; antiarteriosclerotic; nephrotropic;
 KW ophthalmological; hepatotropic; antithyroid; antiinflammatory; antitumor;
 KW gastrointestinal; antirheumatic; osteopathic; antiarthritic; hemostatic;
 KW antipsoriatic; dermatological; immunosuppressive; antibacterial.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 802..1124
 FT /note= "catalytic domain; specifically claimed fragment"
 XX
 PN WO200172778-A2.
 XX
 PD 04-OCT-2001.
 XX
 XX 20-MAR-2001; 2001WO-US08853.
 XX
 XX 29-MAR-2000; 2000US-192920P.
 XX
 PA (BADI) BASF AG.
 XX
 PI Bump NJ, Arnold LD, Dixon RW, Hoeffken HW, Allen K, Bellamacina C;
 DR WPI; 2001-648437/74.
 XX
 PT Crystalline polypeptide useful for identifying inhibitors of a Tie-2
 PT protein as well as determining the three dimensional structure of a
 PT polypeptide comprising the catalytic domain of a Tie-2 polypeptide -
 XX
 PS Claim 6; Fig 1; 242pp; English.
 CC The invention relates to a crystalline polypeptide, comprising the
 CC catalytic domain of a receptor tyrosine kinase Tie-2 protein. The
 CC crystalline forms are useful for identifying inhibitors of a Tie-2
 CC protein as well as determining the three dimensional structure of a
 CC the catalytic domain of a Tie-2 polypeptide. A Tie-2 inhibitor may be
 CC used to treat a Tie-2 dependent condition in a patient (especially a
 CC human), where the condition is characterized by excessive vascular
 CC proliferation e.g. a hyperproliferative disorder, cancer (e.g. sarcoma,
 CC osteoma, melanoma, lymphoma, and leukemia), a cardiovascular condition
 CC (e.g. atherosclerosis, ischemia, anemia, and vascular leakage disorders),
 CC an ocular condition (myopia, chronic retinal detachment, conjunctivitis,
 CC retinopathy, and macular degeneration), von Hippel Lindau disease,
 CC pemphigoid, psoriasis, Paget's disease, polycystic kidney disease,
 CC fibrosis, sarcoidosis, cirrhosis, thyroiditis, Osler-Weber-Rendu disease,
 CC chronic inflammation, synovitis, inflammatory bowel disease, Crohn's
 CC disease, rheumatoid arthritis, osteoarthritis, psoriatic arthritis, and
 CC ulcer or sepsis, especially where the disorder involves aberrant
 CC endothelial-peri-endothelial interactions. The Tie-2 inhibitor may be
 CC used to decrease fertility, and promote angiogenesis or vasculogenesis
 CC (in combination with a pro-angiogenic growth factor). The present
 CC sequence represents the human Tie-2 protein sequence.
 XX
 SQ Sequence 1124 AA;
 Query Match 61.4%; Score 35; DB 22; Length 1124;
 Best local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CATDIKGAEC 10
 ||| ||| :|
 Db 289 CATGWKGLQC 298

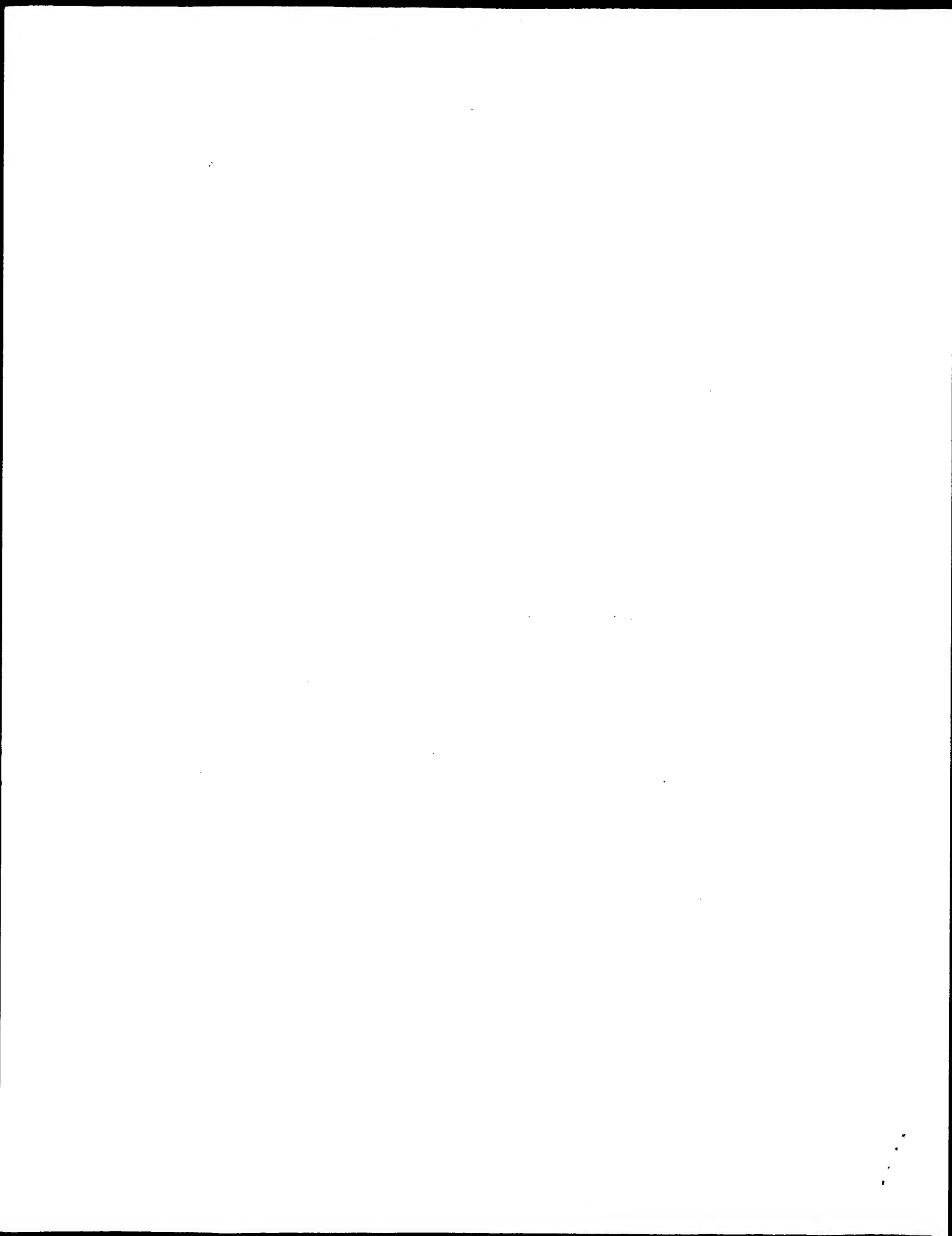
RESULT 15
 ABB95463
 ID ABB95463 standard; Protein; 1124 AA.
 XX
 AC ABB95463;
 XX
 DT 19-JUL-2002 (first entry)
 XX
 DE Human angiogenesis related protein PRO734 SEQ ID NO: 82.
 XX
 KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
 KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
 KW cardiac; cytostatic; antiangiogenic; hypotensive; vulnery;
 KW antiarteriosclerotic.
 XX
 OS Homo sapiens.
 XX
 PN WO200208284-A2.
 XX
 PD 31-JAN-2002.
 XX
 XX 09-JUL-2001; 2001WO-US21735.
 XX
 XX 20-JUL-2000; 2000US-219556P.
 XX 25-JUL-2000; 2000US-220624P.
 XX 25-JUL-2000; 2000US-220664P.
 XX 28-JUL-2000; 2000WO-US20710.
 XX 02-AUG-2000; 2000US-222695P.
 XX 17-AUG-2000; 2000US-0643657.
 XX 23-AUG-2000; 2000WO-US23522.
 XX 24-AUG-2000; 2000WO-US23328.
 XX 07-SEP-2000; 2000US-230978P.
 XX 15-SEP-2000; 2000US-000000P.
 XX 18-SEP-2000; 2000US-0664610.
 XX 18-SEP-2000; 2000US-0665350.
 XX 24-OCT-2000; 2000US-242922P.
 XX 08-NOV-2000; 2000US-0709238.
 XX 08-NOV-2000; 2000WO-US30952.
 XX 10-NOV-2000; 2000WO-US30873.
 XX 01-DEC-2000; 2000WO-US32678.
 XX 20-DEC-2000; 2000US-0747259.
 XX 20-DEC-2000; 2000WO-US34956.
 XX 22-JAN-2001; 2001US-0767609.
 XX 28-FEB-2001; 2001US-0796498.
 XX 28-FEB-2001; 2001WO-US06520.
 XX 01-MAR-2001; 2001WO-US06666.
 XX 09-MAR-2001; 2001US-0802706.
 XX 14-MAR-2001; 2001US-0808689.
 XX 22-MAR-2001; 2001US-0816744.
 XX 05-APR-2001; 2001US-0828366.
 XX 10-MAY-2001; 2001US-0854208.
 XX 10-MAY-2001; 2001US-0854280.
 XX 25-MAY-2001; 2001US-0866028.
 XX 25-MAY-2001; 2001US-0866034.
 XX 30-MAY-2001; 2001WO-US17092.
 XX 30-MAY-2001; 2001US-0870574.
 XX 01-JUN-2001; 2001WO-US17443.
 XX 20-JUN-2001; 2001WO-US17800.
 XX 28-JUN-2001; 2001WO-US19692.
 XX
 XX (GETH) GENENTECH INC.
 XX (BAKE/) BAKER K P.
 XX (FER/) FERRARA N.
 XX (GERB/) GERBER H.
 XX (GERR/) GERRITSEN M E.
 XX (GODD/) GODDARD A.
 XX (GODO/) GODOWSKI P J.
 XX (GURN/) GURNEY A L.
 XX (HILL/) HILLAN K J.
 XX (MARS/) MARSTERS S A.
 XX (PANU/) PAN J.

PA (PAONI/) PAONI N F.
 PA (STEP/) STEPHAN J F.
 PA (WATA/) WATANABE C K.
 PA (WILL/) WILLIAMS P M.
 PA (WOOD/) WOOD W I.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
 PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI; 2002-171999/22.
 DR N-PSDB; ABL95601.
 XX
 PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
 PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
 PT infarction), endothelial or angiogenic disorders in a mammal -
 PT
 PS Claim 11; Fig 82; 567pp; English.
 XX
 CC The present invention provides the protein and coding sequences of human
 CC PRO proteins. These are useful for treating or diagnosing a
 CC cardiovascular, endothelial or angiogenic disorder, including cardiac
 CC hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The present sequence is a PRO protein of the invention.
 XX
 SQ Sequence 1124 AA;

 Query Match 61.4%; Score 35; DB 23; Length 1124;
 Best Local Similarity 60.0%; Pred. No. 1.5e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 QY 1 CATDIKGAEC 10
 ||| || : |
 Db 289 CATGWKGLQC 298

 Search completed: November 9, 2002, 14:01:18
 Job time : 34.8462 secs



XX Claim 11; Page 6235-6236; 9803pp; English.
 PS AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patients own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated Ps,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAH77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 XX
 SQ Sequence 62 AA;
 Query Match 89.2%; Score 33; DB 22; Length 62;
 Best Local Similarity 83.3%; Pred. No. 68;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CKGAIC 6
 Db 37 CKGVIC 42
 RESULT 4
 AAG08770
 ID AAG08770 standard; Protein; 122 AA.
 AC AAG08770;
 DT 17-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 6439.
 KW Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 OS Arabidopsis thaliana.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 PF 25-FEB-2000; 2000EP-0301439.
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
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PR	16-AUG-1999;	99US-0149368.
PR	17-AUG-1999;	99US-0149175.
PR	18-AUG-1999;	99US-0149426.
PR	20-AUG-1999;	99US-0149722.
PR	20-AUG-1999;	99US-0149723.
PR	20-AUG-1999;	99US-0149929.
PR	23-AUG-1999;	99US-0149902.
PR	23-AUG-1999;	99US-0149930.
PR	25-AUG-1999;	99US-0150566.
PR	26-AUG-1999;	99US-0150884.
PR	27-AUG-1999;	99US-0151065.
PR	27-AUG-1999;	99US-0151066.
PR	27-AUG-1999;	99US-0151080.
PR	30-AUG-1999;	99US-0151303.
PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
PR	15-SEP-1999;	99US-0154018.
PR	16-SEP-1999;	99US-0154039.
PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	21-OCT-1999;	99US-0160815.
PR	22-OCT-1999;	99US-0160980.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	22-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	26-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.

Query Match 89.2%; Score 33; DB 21; Length 125;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| | | | |
Db 94 CKGGIC 99

RESULT 8
RAY97725
ID AAY97725 standard; Protein; 461 AA.

AC AAY97725;

DT 19-JUN-2001 (first entry)

DE NS1 protein sequence.

KW Fusion nucleic acid library; Rep protein; tumour cell; apoptosis;
KW nucleic acid modification enzyme; cell death; decreased cell growth;
KW protein-protein interaction detection; cell division; cancer therapy;
KW protein drug discovery; pharmacogenetics; NS1 protein.

OS Goose parvovirus.

PN WO200114539-A2.

PD 01-MAR-2001.

XX 18-AUG-2000; 2000WO-US22906.

XX 20-AUG-1999; 99US-0150004.

PR 02-JUN-2000; 2000US-0209130.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX LI M;

XX WPI; 2001-218443/22.

DR N-PSDB; AAA91315.

XX New library of fusion nucleic acids each encoding a Rep protein
PT recognized by a nucleic acid modification enzyme and a candidate
PT protein, useful for detecting protein-protein interactions, protein
PT drug discovery or pharmacogenetics

PS Disclosure; Fig 31; 106pp; English.

XX This sequence is the goose parvovirus NS1 protein.
CC The invention relates to a library of fusion nucleic acids, each encoding
CC a Rep protein, a candidate protein, a presentation structure, a targeting
CC sequence or a label. The Rep protein is a nucleic acid modification
CC enzyme. The random or directed libraries (including the cDNA libraries)
CC can be introduced into any tumour cell, and peptides identified which by
CC themselves induce apoptosis, cell death, loss of cell division or
CC decreased cell growth. The methods and compositions may also be used to
CC detect protein-protein interactions, protein drug discovery,
CC particularly for protein drugs that interact with targets on cell
CC surfaces, to discover DNA or nucleic acid binding proteins, using
CC nucleic acids as targets, to screen for nucleic acid modification enzymes
CC with decreased toxicity for the host cells, to identify or generate Rep
CC proteins with decreased toxicity, improved enzyme attachment sequences
CC for use in expression vectors and in pharmacogenetic studies. The method
CC is useful in cancer therapy and in killing tumour cells. The methods can
CC be combined with other cancer therapeutics (drugs or radiation) to
CC sensitize cells and thus induce rapid and specific apoptosis, cell death,
CC loss of cell division or decreased cell growth after exposure to a
CC secondary agent.

XX Sequence 461 AA;

Query Match 89.2%; Score 33; DB 22; Length 461;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| | | | |
Db 241 CKGSVC 246

RESULT 9
AAE22892
ID AAE22892 standard; Protein; 461 AA.

XX AAE22892;

XX 09-AUG-2002 (first entry)

XX Goose parvovirus NS1 protein.

KW Nucleic acid/protein conjugate; NAP; nucleic acid modification; NAM; EAS;
KW enzyme attachment sequence; cancer therapy; protein-protein interaction;
KW drug discovery; NS1 protein; gene therapy; cytostatic.

OS Goose parvovirus.

XX Key Location/Qualifiers
FH Misc-difference 68
FT /note= "Encoded by ATT"

XX WO200222826-A2.

XX 21-MAR-2002.

XX 14-SEP-2001; 2001WO-US28702.

XX 14-SEP-2000; 2000US-232960P.

XX (XENC-) XENCOR INC.

XX Li M, Melander C, Liu H;

XX WPI; 2002-393969/42.

DR N-PSDB; AAD36286.

XX Library of nucleic acid/protein conjugates, has a fusion of nucleic
PT acid modification enzyme and candidate compound, and expression vector
PT having a fusion of nucleic acids encoding NAM enzyme and the compound

PS Disclosure; Fig 31; 96pp; English.

XX The present invention relates to genetic libraries of nucleic acid/
CC protein (NAP) conjugates comprising a fusion polypeptide (with a nucleic
CC acid modification (NAM) enzyme (E) and candidate compound), an expression
CC vector (with a fusion of nucleic acids encoding the enzyme and candidate
CC protein respectively), an enzyme attachment sequence (EAS; RNA sequence),
CC where the candidate compound and candidate protein are different and EAS
CC and the enzyme are covalently linked. The NAP conjugates are useful in
CC screens to assay binding to target molecules and/or to screen candidate
CC agents for the ability to modulate the activity of the target molecule.
CC They are useful in cancer therapy. Sequences of the invention are also
CC useful to detect protein-protein interaction, in drug discovery, to
CC discover DNA or nucleic acid binding proteins, using nucleic acids as
CC the targets and to screen for NAM enzymes with decreased toxicity for
CC host cells (specifically Rep proteins with reduced toxicity). NAP
CC conjugates are also useful in pharmacogenomic studies, for screening
CC bioactive agents on surface cells, viruses and microbial organisms. They
CC are also useful for screening proteins causing phenotypic changes such
CC as overproduction or inhibition of protein expression, or proteins that
CC alter attachment, infectivity, etc. of the virus. Sequences of the
CC invention are also used in gene therapy. The present sequence is
CC Goose parvovirus NS1 protein used in the invention.

XX Sequence 461 AA;

Query Match 89.2%; Score 33; DB 23; Length 461;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGAIC 6
| | | | |
Db 241 CKGSVC 246

RESULT 10

AAR85384
ID AAR85384 standard; Protein; 626 AA.

XX AAR85384;

XX 09-MAY-1996 (first entry)

XX Barbary duck parvovirus fragment ORF1 encoded non-structural protein.

XX Barbary duck; parvovirus; open reading frame; non-structural; VP1; VP2;
XX liver extract; virus particle; vector; host cell; attenuated; geese.

XX Barbary duck parvovirus.

XX Key Location/Qualifiers

XX Misc-difference 213 /note= "encoded by GTA"

XX FR2718151-A1.

XX 06-OCT-1995.

XX 03-MAR-1995; 95FR-0002515.

XX 03-MAR-1994; 94HU-0000634.

XX (SNFI) PHYLAXIA-SANOI OLTOANYAGTERMELO RT.

XX Erdei J, Kisari J, Nagy J, Zadori Z;

XX WPI; 1995-345564/45.

XX N-PSDB; AAT01190.

XX Nucleic acid sequence from Barbary duck parvovirus - related
XX vectors, transformed cells, proteins etc., useful diagnostically and
XX in protective vaccines

XX Claim 2; Fig 3; 39pp; French.

XX The sequence of the non-structural protein encoded by the open reading
XX frame (ORF) 1 contained in a fragment from the Barbary duck parvovirus
XX strain FM. The fragment contains 3 ORFs, with ORF3 being internal to
XX ORF2, encoding a non-structural, the VP1 and VP2 proteins respectively.
XX The virus was isolated from a 13 day old duck that had died of Barbary
XX duck parvovirus infection, by incubating liver extracts injected into
XX embryonated duck eggs. The DNA was isolated from the resulting 20-25 nm
XX viral particles. The DNA sequences encoding the non-structural,
XX VP1 (AAR85385) or VP2 (AAR85386) proteins can be used to construct viral
XX vectors, host cells or attenuated parvoviruses for use as vaccines to
XX protect Barbary ducks and geese.

XX Sequence 626 AA;

Query Match 89.28; Score 33; DB 16; Length 626;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGAIC 6
| | | | |
Db 406 CKGSVC 411

RESULT 11

AA97724
ID AA97724 standard; Protein; 626 AA.

XX

AC AAY97724;

XX 19-JUN-2001 (first entry)

XX NS1 protein sequence.

XX Fusion nucleic acid library; Rep protein; tumour cell; apoptosis;
XX nucleic acid modification enzyme; cell death; decreased cell growth;
XX protein-protein interaction detection; cell division; cancer therapy;
XX protein drug discovery; pharmacogenetics; NS1 protein; ds.

XX Muscovy duck parvovirus.

XX WO200114539-A2.

XX 01-MAR-2001.

XX 18-AUG-2000; 2000WO-US22906.

XX 20-AUG-1999; 99US-0150004.

XX 02-JUN-2000; 2000US-0209130.

XX (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.

XX Li M;

XX WPI; 2001-218443/22.

XX N-PSDB; AAA91314.

XX New library of fusion nucleic acids each encoding a Rep protein
XX recognized by a nucleic acid modification enzyme and a candidate
XX protein, useful for detecting protein-protein interactions, protein
XX drug discovery or pharmacogenetics -

XX Disclosure; Fig 29; 106pp; English.

XX This sequence is the muscovy duck parvovirus NS1 protein.

XX The invention relates to a library of fusion nucleic acids, each encoding
XX a Rep protein, a candidate protein, a presentation structure, a targeting
XX sequence or a label. The Rep protein is a nucleic acid modification
XX enzyme. The random or directed libraries (including the cDNA libraries)
XX can be introduced into any tumour cell, and peptides identified which by
XX themselves induce apoptosis, cell death, loss of cell division or
XX decreased cell growth. The methods and compositions may also be used to
XX detect protein-protein interactions, protein drug discovery,
XX particularly for protein drugs that interact with targets on cell
XX surfaces, to discover DNA or nucleic acid binding proteins, using
XX nucleic acids as targets, to screen for nucleic acid modification enzymes
XX with decreased toxicity for the host cells, to identify or generate Rep
XX proteins with decreased toxicity, improved enzyme attachment sequences
XX for use in expression vectors and in pharmacogenetic studies. The method
XX is useful in cancer therapy and in killing tumour cells. The methods can
XX be combined with other cancer therapeutics (drugs or radiation) to
XX sensitize cells and thus induce rapid and specific apoptosis, cell death,
XX loss of cell division or decreased cell growth after exposure to a
XX secondary agent.

XX Sequence 626 AA;

Query Match 89.2%; Score 33; DB 22; Length 626;
Best Local Similarity 66.7%; Pred. No. 4.7e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGAIC 6
| | | | |
Db 406 CKGSVC 411

RESULT 12

AAE22891

ID AAE22891 standard; Protein; 626 AA.

XX

AC AAE22891;
 DT 09-AUG-2002 (first entry)
 DE Muscovy duck parvovirus NS1 protein.
 XX
 DE Nucleic acid/protein conjugate; NAP; nucleic acid modification; NAM; EAS;
 XX enzyme attachment sequence; cancer therapy; protein-protein interaction;
 KW drug discovery; NS1 protein; gene therapy; cytostatic.
 KW
 XX Muscovy duck parvovirus.
 OS
 XX WO200222826-A2.
 XX
 PN 21-MAR-2002.
 XX
 PD 14-SEP-2001; 2001WO-US28702.
 XX
 PF 14-SEP-2000; 2000US-232960P.
 XX
 PR (XENC-) XENCOR INC.
 XX
 PA Li M, Melander C, Liu H;
 XX
 PI WPI; 2002-393969/42.
 XX
 DR N-PSDB; AAD36285.
 DR
 XX Library of nucleic acid/protein conjugates, has a fusion of nucleic
 PT acid modification enzyme and candidate compound, and expression vector
 PT having a fusion of nucleic acids encoding NAM enzyme and the compound
 PT
 XX Disclosure; Fig 29; 96pp; English.
 PS
 XX The present invention relates to genetic libraries of nucleic acid/
 CC protein (NAP) conjugates comprising a fusion polypeptide (with a nucleic
 CC acid modification (NAM) enzyme (E) and candidate compound), an expression
 CC vector (with a fusion of nucleic acids encoding the enzyme and candidate
 CC protein respectively), an enzyme attachment sequence (EAS; RNA sequence),
 CC where the candidate compound and candidate protein are different and EAS
 CC and the enzyme are covalently linked. The NAP conjugates are useful in
 CC screens to assay binding to target molecules and/or to screen candidate
 CC agents for the ability to modulate the activity of the target molecule.
 CC They are useful in cancer therapy. Sequences of the invention are also
 CC useful to detect protein-protein interaction, in drug discovery, to
 CC discover DNA or nucleic acid binding proteins, using nucleic acids as
 CC the targets and to screen for NAM enzymes with reduced toxicity for
 CC host cells (specifically Rep proteins with reduced toxicity). NAP
 CC conjugates are also useful in pharmacogenomic studies, for screening
 CC bioactive agents on surface cells, viruses and microbial organisms. They
 CC are also useful for screening proteins causing phenotypic changes such
 CC as overproduction or inhibition of protein expression, or proteins that
 CC alter attachment, infectivity, etc. of the virus. Sequences of the
 CC invention are also used in gene therapy. The present sequence is
 CC muscovy duck parvovirus NS1 protein used in the invention.
 XX
 XX Sequence 626 AA;
 SQ
 Query Match 89.2%; Score 33; DB 23; Length 626;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CKGAIC 6
 |||:|
 Db 406 CKGSVC 411
 RESULT 13
 AAY97722
 ID AAY97722 standard; Protein; 627 AA.
 XX
 XX AAY97722;
 AC
 XX 19-JUN-2001 (first entry)
 Rep protein sequence.
 XX
 XX Fusion nucleic acid library; Rep protein; tumour cell; apoptosis;
 KW nucleic acid modification enzyme; cell death; decreased cell growth;
 KW protein-protein interaction detection; cell division; cancer therapy;
 KW protein drug discovery; pharmacogenetics.
 XX
 OS
 XX
 XX
 XX WO200114539-A2.
 XX
 PN 01-MAR-2001.
 XX
 PD 18-AUG-2000; 2000WO-US22906.
 XX
 PF 20-AUG-1999; 99US-0150004.
 XX
 PR 02-JUN-2000; 2000US-0209130.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX
 PI Li M;
 XX
 WPI; 2001-218443/22.
 DR
 DR N-PSDB; AAA91312.
 XX
 XX New library of fusion nucleic acids each encoding a Rep protein
 PT recognized by a nucleic acid modification enzyme and a candidate
 PT protein, useful for detecting protein-protein interactions, protein
 PT drug discovery or pharmacogenetics -
 PT
 XX Disclosure; Fig 25; 106pp; English.
 PS
 XX This sequence is the barbarie duck parvovirus Rep protein.
 CC The invention relates to a library of fusion nucleic acids, each encoding
 CC a Rep protein, a candidate protein, a presentation structure, a targeting
 CC sequence or a label. The Rep protein is a nucleic acid modification
 CC enzyme. The random or directed libraries (including the cDNA libraries)
 CC can be introduced into any tumour cell, and peptides identified which by
 CC themselves induce apoptosis, cell death, loss of cell division or
 CC decreased cell growth. The methods and compositions may also be used to
 CC detect protein-protein interactions, protein drug discovery,
 CC particularly for protein drugs that interact with targets on cell
 CC surfaces, to discover DNA or nucleic acid binding proteins, using
 CC nucleic acids as targets, to screen for nucleic acid modification enzymes
 CC with decreased toxicity for the host cells, to identify or generate Rep
 CC proteins with decreased toxicity, improved enzyme attachment sequences
 CC for use in expression vectors and in pharmacogenetic studies. The method
 CC is useful in cancer therapy and in killing tumour cells. The methods can
 CC be combined with other cancer therapeutics (drugs or radiation) to
 CC sensitize cells and thus induce rapid and specific apoptosis, cell death,
 CC loss of cell division or decreased cell growth after exposure to a
 CC secondary agent.
 XX
 XX Sequence 627 AA;
 SQ
 Query Match 89.2%; Score 33; DB 22; Length 627;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CKGAIC 6
 |||:|
 Db 407 CKGSVC 412
 RESULT 14
 AAY97723
 ID AAY97723 standard; Protein; 627 AA.
 XX
 XX AAY97723;
 AC
 XX 19-JUN-2001 (first entry)

XX DE Rep protein sequence.
 XX XX Fusion nucleic acid library; Rep protein; tumour cell; apoptosis;
 KW nucleic acid modification enzyme; cell death; decreased cell growth;
 KW protein-protein interaction detection; cell division; cancer therapy;
 KW protein drug discovery; pharmacogenetics.
 XX OS Goose parvovirus.
 XX XX WO200114539-A2.
 PN 01-MAR-2001.
 PD 18-AUG-2000; 2000WO-US22906.
 XX 20-AUG-1999; 99US-0150004.
 XX 02-JUN-2000; 2000US-0209130.
 PR (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
 XX PA Li M;
 XX PI WPI; 2001-218443/22.
 XX DR N-PSDB; AAA91313.
 XX PT New library of fusion nucleic acids each encoding a Rep protein
 PT recognized by a nucleic acid modification enzyme and a candidate
 PT protein, useful for detecting protein-protein interactions, protein
 PT drug discovery or pharmacogenetics
 XX PS Disclosure; Fig 27; 106pp; English.
 XX CC This sequence is the goose parvovirus Rep protein.
 CC The invention relates to a library of fusion nucleic acids, each encoding
 CC a Rep protein, a candidate protein, a presentation structure, a targeting
 CC sequence or a label. The Rep protein is a nucleic acid modification
 CC enzyme. The random or directed libraries (including the cDNA libraries)
 CC can be introduced into any tumour cell, and peptides identified which by
 CC themselves induce apoptosis, cell death, loss of cell division or
 CC decreased cell growth. The methods and compositions may also be used to
 CC detect protein-protein interactions, protein drug discovery.
 CC particularly for protein drugs that interact with targets on cell
 CC surfaces, to discover DNA or nucleic acid binding proteins, using
 CC nucleic acids as targets, to screen for nucleic acid modification enzymes
 CC with decreased toxicity for the host cells, to identify or generate Rep
 CC proteins with decreased toxicity, improved enzyme attachment sequences
 CC for use in expression vectors and in pharmacogenetic studies. The method
 CC is useful in cancer therapy and in killing tumour cells. The methods can
 CC be combined with other cancer therapeutics (drugs or radiation) to
 CC sensitize cells and thus induce rapid and specific apoptosis, cell death,
 CC loss of cell division or decreased cell growth after exposure to a
 CC secondary agent.
 XX XX Sequence 627 AA;
 SQ Query Match 89.2%; Score 33; DB 22; Length 627;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CKGAIC 6
 |||::|
 Db 407 CKGSVC 412
 RESULT 15
 AAEE22889
 ID AAEE22889 standard; Protein; 627 AA.
 XX AC AAEE22889;
 XX DT 09-AUG-2002 (first entry)
 XX

DE DE Barbarie duck parvovirus Rep protein.
 XX XX Nucleic acid/protein conjugate; NAP; nucleic acid modification; NAM; EAS;
 KW enzyme attachment sequence; cancer therapy; protein-protein interaction;
 KW drug discovery; Rep protein; gene therapy; cytostatic.
 XX OS Barbarie duck parvovirus.
 XX XX Key Location/Qualifiers
 FH Misc-difference 262 /note= "Encoded by ANC"
 FT WO200222826-A2.
 PN 21-MAR-2002.
 PD 14-SEP-2001; 2001WO-US28702.
 XX 14-SEP-2000; 2000US-232960P.
 PR (XENC-) XENCOR INC.
 XX Li M, Melander C, Liu H;
 XX WPI; 2002-393969/42.
 XX DR N-PSDB; AAD36283.
 XX PT Library of nucleic acid/protein conjugates, has a fusion of nucleic
 PT acid modification enzyme and candidate compound, and expression vector
 PT having a fusion of nucleic acids encoding NAM enzyme and the compound
 XX PS Disclosure; Fig 25; 96pp; English.
 XX CC The present invention relates to genetic libraries of nucleic acid/
 CC protein (NAP) conjugates comprising a fusion polypeptide (with a nucleic
 CC acid modification (NAM) enzyme (E) and candidate compound), an expression
 CC vector (with a fusion of nucleic acids encoding the enzyme and candidate
 CC protein respectively), an enzyme attachment sequence (EAS; RNA sequence),
 CC where the candidate compound and candidate protein are different and EAS
 CC and the enzyme are covalently linked. The NAP conjugates are useful in
 CC screens to assay binding to target molecules and/or to screen candidate
 CC agents for the ability to modulate the activity of the target molecule.
 CC They are useful in cancer therapy. Sequences of the invention are also
 CC useful to detect protein-protein interaction, in drug discovery, to
 CC discover DNA or nucleic acid binding proteins, using nucleic acids as
 CC the targets and to screen for NAM enzymes with decreased toxicity for
 CC host cells (specifically Rep proteins with reduced toxicity). NAP
 CC conjugates are also useful in pharmacogenomic studies, for screening
 CC bioactive agents on surface cells, viruses and microbial organisms. They
 CC are also useful for screening proteins causing phenotypic changes such
 CC as overproduction or inhibition of protein expression, or proteins that
 CC alter attachment, infectivity, etc. of the virus. Sequences of the
 CC invention are also used in gene therapy. The present sequence is
 CC Barbarie duck parvovirus Rep protein.
 XX XX Sequence 627 AA;
 SQ Query Match 89.2%; Score 33; DB 23; Length 627;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CKGAIC 6
 |||::|
 Db 407 CKGSVC 412

Search completed: November 9, 2002, 14:01:19
 Job time : 21.3077 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:04 ; Search time 26.5385 Seconds
(without alignments)
77.641 Million cell updates/sec

Title: US-09-632-748-4

Perfect score: 57

Sequence: 1 CVGSNKGAIK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-rvirus:*
16: sp-bacteriap:*
17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	41	71.9	76	10 Q9LRD8	Q9LRD8 brassica ca
2	40	70.2	284	16 Q9PD24	Q9PD24 xylella fas
3	39	68.4	33	4 Q9UC33	Q9UC33 homo sapien
4	39	68.4	49	6 Q97917	Q97917 bos taurus
5	39	68.4	79	11 Q35463	Q35463 cricetus
6	39	68.4	80	5 Q9BP85	Q9BP85 conus arena
7	39	68.4	82	4 Q16014	Q16014 homo sapien
8	39	68.4	82	4 Q16019	Q16019 homo sapien
9	39	68.4	82	4 Q16020	Q16020 homo sapien
10	39	68.4	82	4 Q16020	Q16020 homo sapien
11	39	68.4	97	4 Q13778	Q13778 homo sapien
12	39	68.4	513	5 Q95SK6	Q95SK6 drosophila
13	39	68.4	534	13 Q93296	Q93296 gallus gall
14	39	68.4	569	13 Q9PVL1	Q9PVL1 gallus gall
15	39	68.4	607	11 Q99K32	Q99K32 mus musculus
16	39	68.4	693	13 Q98SG0	Q98SG0 xenopus lae

17	39	68.4	695	6	Q95KN7	Q95KN7 macaca fasc
18	39	68.4	695	11	Q60496	Q60496 cavia sp. p
19	39	68.4	695	11	P97487	P97487 mus musculus
20	39	68.4	695	13	Q9DGJ8	Q9DGJ8 gallus gall
21	39	68.4	695	13	Q98SF9	Q98SF9 xenopus lae
22	39	68.4	699	13	O57394	O57394 narke japon
23	39	68.4	737	13	O93279	O93279 fugu rubrip
24	39	68.4	747	13	O91963	O91963 xenopus. ap
25	39	68.4	751	13	O9DGJ7	O9DGJ7 gallus gall
26	39	68.4	770	6	Q9TU10	Q9TU10 sus scrofa
27	39	68.4	780	13	O73683	O73683 tetraodon f
28	38	66.7	372	5	Q21756	Q21756 caenorhabdi
29	38	66.7	1136	12	O8V6X1	O8V6X1 iris yellow
30	37	64.9	89	5	O45563	O45563 caenorhabdi
31	37	64.9	357	10	Q9XE30	Q9XE30 oryza sativ
32	37	64.9	384	2	P96478	P96478 streptococc
33	37	64.9	560	5	O61085	O61085 dictyosteli
34	37	64.9	1298	5	O9V714	O9V714 drosophila
35	37	64.9	1361	5	O9NGV2	O9NGV2 drosophila
36	37	64.9	4601	5	Q9V383	Q9V383 drosophila
37	36	63.2	239	13	O8UUI7	O8UUI7 brachydanio
38	36	63.2	389	3	Q9C3Z8	Q9C3Z8 volvariella
39	36	63.2	584	2	Q9L4Q6	Q9L4Q6 clostridium
40	36	63.2	694	13	Q8UUR9	Q8UUR9 brachydanio
41	36	63.2	1088	17	O28333	O28333 archaeglob
42	36	63.2	1555	5	Q9U3S7	Q9U3S7 caenorhabdi
43	36	63.2	1973	5	Q17465	Q17465 caenorhabdi
44	35	61.4	30	4	Q9UCA9	Q9UCA9 homo sapien
45	35	61.4	119	4	Q9NR68	Q9NR68 homo sapien

ALIGNMENTS

RESULT 1

Q9LRD8 PRELIMINARY; PRT; 76 AA.
ID Q9LRD8;
AC Q9LRD8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE S locus protein 11-34 (Fragment).
GN SP11-34.
OS Brassica campestris (Field mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3711;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S34(S-5J);
RX MEDLINE=20273842; PubMed=10812061;
RA Watanabe M., Ito A., Takada Y., Ninomiya C., Kakizaki T., Takahata Y.,
RA Hatakeyama K., Hinata K., Suzuki G., Takasaki T., Satta Y., Shiba H.,
RA Takayama S., Isogai A.;
RT "Highly divergent sequences of the pollen self-incompatibility (S)
gene in class-I S haplotypes of Brassica campestris (syn. rapa) L.";
RL FEBS Lett. 473:139-144(2000).
DR EMBL; AB039758; BAA96396.1; -.
FT NON_TER 1
SQ SEQUENCE 76 AA; 8730 MW; 4018830CF39600A6 CRC64;

Query Match 71.9%; Score 41; DB 10; Length 76;
Best Local Similarity 70.0%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVGSNKGAIK 10
Db 56 CVGSRRKHALC 65
||||| | | |

RESULT 2
Q9PD24

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ID Q9PD24 PRELIMINARY; PRT; 284 AA.
AC Q9PD24;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Phage-related protein.
GN XFL555.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Coutinho L.L., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Falcinani A.P., Ferreira A.J.S., Ferreira V.C.A., Docena C., El-Dorri H.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuranae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lenos E.G.M., Lenos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Queglio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshukho M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa."
RL Nature 406:151-159(2000).
DR EMBL; AE003985; AAF84364.1; -.
DR HSSP; P03700; 1AE9.
DR InterPro; IPR002104; Phage_integrase.
DR InterPro; IPR004107; Phage_integr_N.
DR Pfam; PF00589; Phage_integrase; 1.
DR Pfam; PF02899; Phage_integr_N; 1.
KW Complete proteome.
SQ SEQUENCE 284 AA; 32141 MW; 2D4971341AF3F048 CRC64;

Query Match 70.2%; Score 40; DB 16; Length 284;
Best Local Similarity 60.0%; Pred. No. 6.9; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;

QY 1 CVGSNKGATC 10
DB 248 CVGDDGALC 257
||| : ||:|

RESULT 3
Q9UC33 PRELIMINARY; PRT; 33 AA.
AC Q9UC33;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN [1]
RP SEQUENCE.
RX MEDLINE=93024877; PubMed=1406936;
RA Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT biological fluids."
RL Nature 359:325-327(1992).
RT HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
SQ SEQUENCE 33 AA; 3674 MW; B1DEFE2F4167ABD0 CRC64;

Query Match 68.4%; Score 39; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 2 VGSNKGAI 9
DB 24 VGSNKGAI 31
|||||||

RESULT 4
O97917 PRELIMINARY; PRT; 49 AA.
AC O97917;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20063685; PubMed=10594237;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
RT level of polymorphism in both intron and exon."
RL Mamm. Genome 10:1142-1145(1999).
DR EMBL; AJ133033; CAB38017.1; -.
DR HSSP; P05067; 1BA4.
DR InterPro; IPR001255; Beta-APP.
DR Pfam; PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 49
SQ SEQUENCE 49 AA; 5183 MW; 6287463F0559BDED CRC64;

Query Match 68.4%; Score 39; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8; Mismatches 0; Indels 0; Gaps 0;
Matches 8; Conservative 0;

QY 2 VGSNKGAI 9
DB 7 VGSNKGAI 14
|||||||

RESULT 5
O35463 PRELIMINARY; PRT; 79 AA.
AC O35463;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Alzheimer's amyloid beta protein (Fragment).
GN BETA APP.
OS Cricetus griseus (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetus.

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OX NCBI_TaxID=10029;
RN [1]
RA SEQUENCE FROM N.A.
RA Sambamurti K., Pinnix I., Gandhi S.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF030413; AAB86608.1; -
DR HSP: P05067; IBA4.
DR InterPro: IPR001255; Beta-APP.
DR PFAM: PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 8538 MW; 37F2C6C3BFF3F597 CRC64;

Query Match 68.4%; Score 39; DB 11; Length 79;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 44 VGSNKGAI 51

RESULT 6
Q9BP85 PRELIMINARY; PRT; 80 AA.
ID Q9BP85
AC Q9BP85
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Conotoxin scaffold VI/VII.
OS Conus arenatus (Sand-dusted cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Caenogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=89451;
RN [1]
RA SEQUENCE FROM N.A.
RA MEDLINE=21105969; PubMed=11158371;
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,
RA Fainzilber M.;
RL "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";
RL Mol. Biol. Evol. 18:120-131(2001).
DR EMBL: AF215053; AAG60481.1; -
DR InterPro: IPR004214; Conotoxin.
DR PFAM: PF02950; Conotoxin; 1.
SQ SEQUENCE 80 AA; 8724 MW; 3A516A7280D9872D CRC64;

Query Match 68.4%; Score 39; DB 5; Length 80;
Best Local Similarity 60.0%; Pred. No. 2.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGAI 10
DB 68 CVGSRPGGLC 77

RESULT 7
Q16014 PRELIMINARY; PRT; 82 AA.
ID Q16014
AC Q16014;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RA MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S60721; AAB26263.2; -
DR HSP: P05067; IBA4.
DR InterPro: IPR001255; Beta-APP.
DR PFAM: PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8972 MW; F534AA5B3EA9230A CRC64;

Query Match 68.4%; Score 39; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 41 VGSNKGAI 48

RESULT 8
Q16019 PRELIMINARY; PRT; 82 AA.
ID Q16019
AC Q16019;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RA MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";

RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
DR EMBL: S61380; AAB26264.2; -
DR HSP: P05067; IBA4.
DR InterPro: IPR001255; Beta-APP.
DR PFAM: PF03494; Beta-APP; 1.
FT NON_TER 1
FT NON_TER 82
SQ SEQUENCE 82 AA; 8938 MW; F534AA50E579230A CRC64;

Query Match 68.4%; Score 39; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
DB 41 VGSNKGAI 48

RESULT 9
Q16020 PRELIMINARY; PRT; 82 AA.
ID Q16020
AC Q16020;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-amyloid peptide (Fragment).
GN BETA APP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA SEQUENCE FROM N.A.
RA MEDLINE=93236601; PubMed=8476439;
RA Denman R.B., Rosenzweig R., Miller D.L.;
RT "A system for studying the effect(s) of familial Alzheimer disease
RT mutations on the processing of the beta-amyloid peptide precursor.";
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RT mutations on the processing of the beta-amyloid peptide precursor.";
 RL Biochem. Biophys. Res. Commun. 192:96-103(1993).
 DR EMBL; S61383; AAB26265.2; -.
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 FT NON_TER 82
 FT NON_TER 82
 SQ SEQUENCE 82 AA; 8882 MW; F534AA5AE5D9230A CRC64;

Query Match 68.4%; Score 39; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 DB 41 VGSNKGAI 48
 |||||

RESULT 10

ID P78438 PRELIMINARY; PRT; 82 AA.
 AC P78438;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Amyloid protein (Beta-amyloid protein) (Fragment).
 GN APP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89392030; PubMed=2675837;
 RA Johnstone E.M., Chaney M.O., Moore R.E., Ward K.E., Norris F.H.,
 RA Little S.P.;
 RT "Alzheimer's disease amyloid peptide is encoded by two exons and shows
 RT similarity to soybean trypsin inhibitor.";
 RL Biochem. Biophys. Res. Commun. 163:1248-1255(1989).
 RN [2]
 RP SEQUENCE OF 19-48 FROM N.A.
 RX MEDLINE=87120329; PubMed=2949367;
 RA Tanzi R.E., Gusella J.F., Watkins P.C., Bruns G.A., George-Hyslop P.,
 RA Van Keuren M.L., Patterson D., Pagan S., Kurnit D.M., Neve R.L.;
 RT "Amyloid beta protein gene: cDNA, mRNA distribution, and genetic
 RT linkage near the Alzheimer locus.";
 RL Science 235:880-884(1987).
 RN [3]
 RP SEQUENCE OF 32-63 FROM N.A.
 RX MEDLINE=93035397; PubMed=1415269;
 RA Kamino K., Orr H.T., Payami H., Wijisman E.M., Alonso M.E., Pulst S.M.,
 RA Anderson L., O'dahl S., Nemens E., White J.A.;
 RT "Linkage and mutational analysis of familial Alzheimer disease
 RT kindreds for the APP gene region.";
 RL Am. J. Hum. Genet. 51:998-1014(1992).
 DR EMBL; M29270; AAA51768.1; -.
 DR EMBL; M29269; AAA51768.1; JOINED.
 DR EMBL; M15532; AAA51564.1; -.
 DR EMBL; S45136; AAB23646.1; -.
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001255; Beta-APP.
 DR Pfam; PF03494; Beta-APP; 1.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 82 AA; 8994 MW; 8DA9BA2B813A070E CRC64;

Query Match 68.4%; Score 39; DB 4; Length 82;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 DB 4Q VGSNKGAI 47
 |||||

RESULT 11

ID Q13778 PRELIMINARY; PRT; 97 AA.
 AC Q13778;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Amyloid protein (AD-AP) (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87120328; PubMed=3810169;
 RA Goldgaber D., Lerman M.I., McBride O.W., Saffiotti U., Gajdusek D.C.;
 RT "Characterization and chromosomal localization of a cDNA encoding
 RT brain amyloid of Alzheimer's disease.";
 RL Science 235:877-880(1987).
 DR EMBL; M15533; AAA35540.1; -.
 DR HSSP; P05067; 1BA4.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta_APP.
 DR Pfam; PF03494; Beta-APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 97 AA; 10884 MW; E528CDB448DE47E CRC64;

Query Match 68.4%; Score 39; DB 4; Length 97;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 DB 22 VGSNKGAI 29
 |||||

RESULT 12

ID Q95SK6 PRELIMINARY; PRT; 513 AA.
 AC Q95SK6;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE GH18278p.
 GN CG15097.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Ceiniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY060733; AAL28281.1; -.
 DR FlyBase; FBgn0034396; CG15097.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR001798; Kelch.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF01344; Kelch; 6.
 DR PROSITE; PS50097; BTB; 1.
 SQ SEQUENCE 513 AA; 57551 MW; 20B9D4F732514834 CRC64;

Query Match 68.4%; Score 39; DB 5; Length 513;
 Best Local Similarity 50.0%; Pred. No. 20;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSKNGAIC 10
I:| | | | |
Db 410 CIGGNDGTMC 419

RESULT 13

ID O93296 PRELIMINARY; PRT; 534 AA.
AC O93296;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Amyloid protein (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98337885; PubMed=9671674;
RA Barnes N.Y., Li L., Yoshikawa K., Schwartz L.M., Oppenheim R.W.,
RA Milligan C.E.;
RT "Increased production of amyloid precursor protein provides a
RT substrate for caspase-3 in dying motoneurons.";
RL J. Neurosci. 18:5869-5880(1998).
DR EMBL: AF042098; AAC25052.1;
DR HSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 534 AA; 60597 MW; FB53ECC2E66D4C92 CRC64;

Query Match 68.4%; Score 39; DB 13; Length 534;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
I:| | | | |
Db 459 VGSNKGAI 466

RESULT 14

ID Q9PVL1 PRELIMINARY; PRT; 569 AA.
AC Q9PVL1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Amyloid protein (Fragment).
GN APP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RA Coulson E.J., Paliga K., Beyreuther K., Masters C.L.;
RT "What the evolution of the amyloid protein precursor supergene family
RT tells us about its function.";
RL Neurochem. Int. 0:0-0(2000).
DR EMBL: AF030341; AAF13698.1;
DR HSP: P05067; 1BA4.
DR InterPro: IPR001868; A4_APP.

DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
FT NON_TER 1
SQ SEQUENCE 569 AA; 64753 MW; OAB8BB851863A19D CRC64;

Query Match 68.4%; Score 39; DB 13; Length 569;

Best Local Similarity 100.0%; Pred. No. 22;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
I:| | | | |
Db 495 VGSNKGAI 502

RESULT 15

ID Q99K32 PRELIMINARY; PRT; 607 AA.
AC Q99K32;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 68.4 kDa protein (Fragment).
GN APP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC005490; AAH05490.1;
DR HSP: P05067; 1AAP.
DR MGD: MGI:88059; App.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR InterPro: IPR002223; Kunitz_BPTI.
DR Pfam: PF02177; A4_EXTRA; 1.
DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICPTASE.
DR ProDom: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
KW Hypothetical protein; Serine protease inhibitor.
FT NON_TER 1
SQ SEQUENCE 607 AA; 68391 MW; BF802214CBA7D172 CRC64;

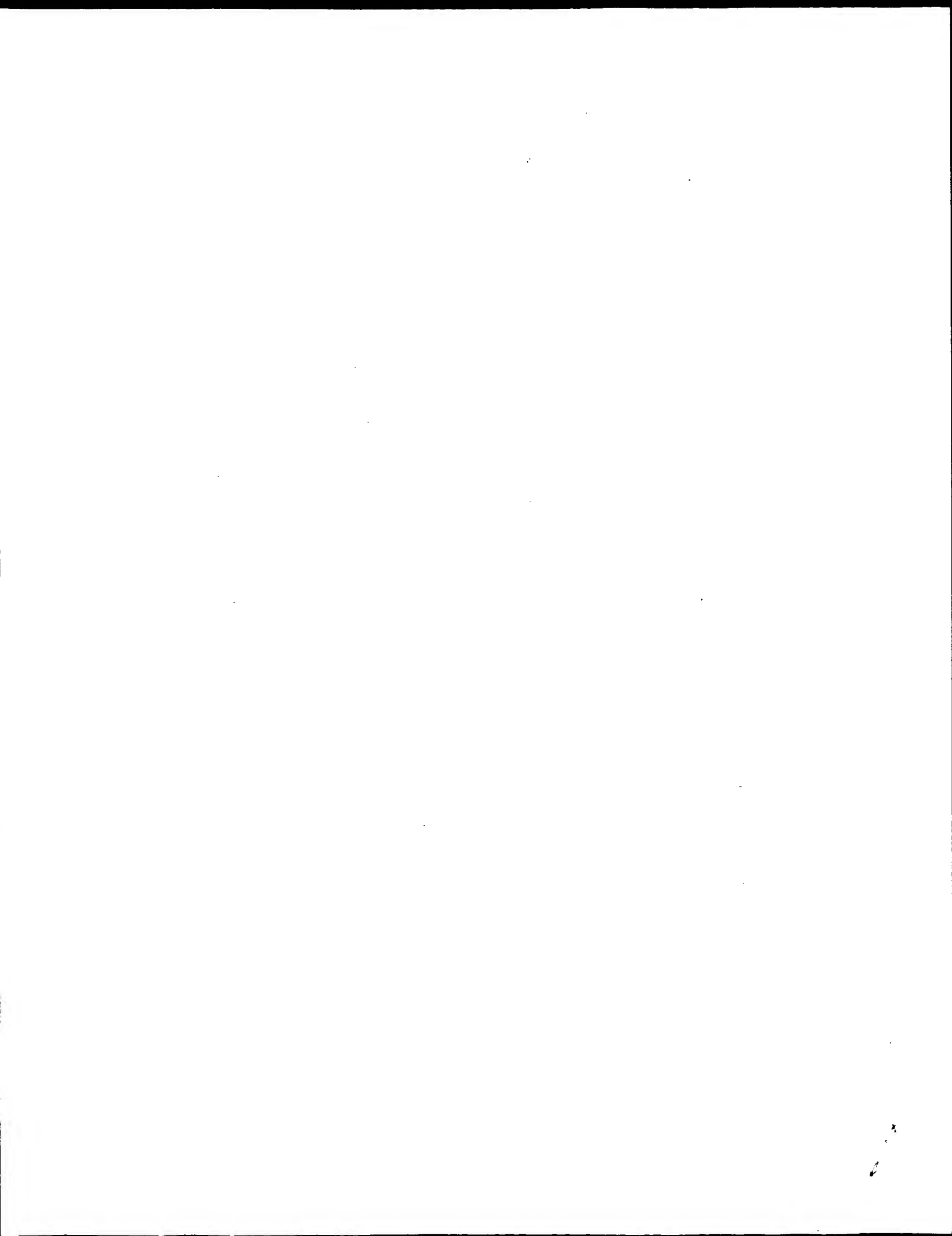
Query Match 68.4%; Score 39; DB 11; Length 607;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
I:| | | | |
Db 532 VGSNKGAI 539

Search completed: November 9, 2002, 14:03:00
Job time : 28.5385 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: November 9, 2002, 13:57:44 ; Search time 7.69231 Seconds
(without alignments)
53.919 Million cell updates/sec

Title: US-09-632-748-4
Perfect score: 57
Sequence: 1 CVGSNKGATC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	39	68.4	57	A4_PIG	Q29023 sus scrofa
2	39	68.4	57	A4_URSA	Q29149 ursus marit
3	39	68.4	58	A4_CANFA	Q28280 canis famli
4	39	68.4	58	A4_RABIT	Q28748 oryctolagus
5	39	68.4	58	A4_SHEEP	Q28757 ovis aries
6	39	68.4	59	A4_BOVIN	Q28053 bos taurus
7	39	68.4	751	A4_SALIC	Q95241 salmieri sci
8	39	68.4	770	A4_HUMAN	P05067 homo sapien
9	39	68.4	770	A4_MOUSE	P12023 mus musculu
10	39	68.4	770	A4_RAT	P08592 rattus norv
11	37	64.9	556	ADEC_ARCFU	Q29999 archaeglob
12	36	63.2	474	PUR1_METHH	Q26742 methanobact
13	35	61.4	260	KLK8_HUMAN	O60259 homo sapien
14	35	61.4	473	FP2_MVTGA	Q25464 mytilus gal
15	34	59.6	316	TAL_HELPJ	Q92105 helicobacte
16	34	59.6	316	TAL_HELPY	P56108 helicobacte
17	34	59.6	457	SYH_BORBU	O51160 borrelia bu
18	34	59.6	661	RDGC_DROME	P40421 drosophila
19	34	59.6	797	DPOM_AGABT	P30322 agaricus bi
20	34	59.6	906	AD22_HUMAN	Q9p0k1 homo sapien
21	34	59.6	1564	N184_SCHPO	Q9p7m8 schizosacch
22	33.5	58.8	1106	DPOD_BOVIN	P28339 bos taurus
23	33.5	58.8	1107	DPOD_HUMAN	P28340 homo sapien
24	33	57.9	30	CXEC_CONCN	P58928 conus conso
25	33	57.9	223	KAD4_HUMAN	P27144 homo sapien
26	33	57.9	223	KAD4_MOUSE	Q9wur9 mus musculu
27	33	57.9	223	KAD4_RAT	Q9wur9 rattus norv
28	33	57.9	303	YNA6_YEAST	P41318 saccharomyc
29	33	57.9	430	PSMR_METJA	Q58576 methanococc
30	33	57.9	497	2A5B_HUMAN	Q15173 homo sapien
31	33	57.9	500	2A5B_RABIT	Q28647 o serine/th
32	33	57.9	704	TRFE_BOVIN	Q29443 bos taurus
33	33	57.9	706	ARN2_HUMAN	Q9hbr2 homo sapien

34	33	57.9	712	1	ARN2_MOUSE	Q61324 mus musculu
35	33	57.9	789	1	ARNT_HUMAN	P27540 homo sapien
36	33	57.9	790	1	ARNT_RABIT	Q02748 oryctolagus
37	33	57.9	791	1	ARNT_MOUSE	P53762 mus musculu
38	33	57.9	800	1	ARNT_RAT	P41739 rattus norv
39	33	57.9	1047	1	RIRI_CHLMU	Q9p193 chlamydia m
40	33	57.9	1047	1	RIRI_CHLTR	O84834 chlamydia t
41	33	57.9	1110	1	VGLM_INSV	Q01260 impatiens n
42	33	57.9	1616	1	YAUD_SCHPO	Q09853 schizosacch
43	32	56.1	161	1	NUDH_RICPR	Q9zdi9 rickettsia
44	32	56.1	199	1	NP25_MOUSE	O9rl08 mus musculu
45	32	56.1	219	1	NP25_RAT	P37805 rattus norv

ALIGNMENTS

RESULT 1
A4_PIG
ID A4_PIG STANDARD; PRT; 57 AA.
AC Q29023;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
DE protein (Beta-APP) (A-beta)] (fragment).
GN APP.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=92017079; PubMed=1656157;
RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
RT "Conservation of the sequence of the Alzheimer's disease amyloid
peptide in dog, polar bear and five other mammals by cross-species
polymerase chain reaction analysis"; RT
RL Brain Res. Mol. Brain Res. 10:299-305(1991).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
G(O) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC EMBL: X56127; CAA39592.1; -.
DR HSP; P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta_APP.
DR Pfam: PF03494; Beta_APP; 1.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
KW Glycoprotein; Amyloid; Neutone; Transmembrane.
FT NON_TER 1 1
FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 34 57 POTENTIAL.
FT NON_TER 57 57
SQ SEQUENCE 57 AA; 6172 MW; 84209D88E8A82DFA CRC64;
Query Match 68.4%; Score 39; DB 1; Length 57;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 |||||
 Db 29 VGSNKGAI 36

RESULT 2

A4_URSWA STANDARD; PRT; 57 AA.
 AC Q29149;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Ursus maritimus (Polar bear) (Thalartos maritimus).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
 OX NCBI_TaxID=29073;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC
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 CC
 CC EMBL; X56128; CAA39593.1; -
 CC HSP; P05067; IBA4.
 CC InterPro; IPR001868; A4_APP.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 34 57 POTENTIAL.
 FT NON_TER 57 57
 SQ SEQUENCE 57 AA; 6172 MW; 84209D88EBA82DFA CRC64;

Query Match 68.4%; Score 39; DB 1; Length 57;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 |||||
 Db 29 VGSNKGAI 36

RESULT 3

A4_CANFA STANDARD; PRT; 58 AA.
 AC Q28280;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 OX NCBI_TaxID=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;
 RT "Conservation of the sequence of the Alzheimer's disease amyloid
 RT peptide in dog, polar bear and five other mammals by cross-species
 RT polymerase chain reaction analysis.";
 RL Brain Res. Mol. Brain Res. 10:299-305(1991).
 CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO
 CC INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN
 CC G(O) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
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 CC
 CC EMBL; X56125; CAA39590.1; -
 CC HSP; P05067; IBA4.
 CC InterPro; IPR001868; A4_APP.
 CC Pfam; PF03494; Beta-APP; 1.
 CC PROSITE; PS00319; A4_EXTRA; PARTIAL.
 CC PROSITE; PS00320; A4_INTRA; PARTIAL.
 CC Glycoprotein; Amyloid; Neurone; Transmembrane.
 FT NON_TER 1 1
 FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
 FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 35 58 POTENTIAL.
 FT NON_TER 58 58
 SQ SEQUENCE 58 AA; 6285 MW; 8469D488A2E12DFA CRC64;
 Query Match 68.4%; Score 39; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 0.81;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 |||||
 Db 30 VGSNKGAI 37

RESULT 4

A4_RABIT STANDARD; PRT; 58 AA.
 AC Q28748;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid
 DE protein (Beta-APP) (A-beta)] (Fragment).
 GN APP.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=92017079; PubMed=1656157;
 RA Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.;

RT "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

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CC -----

DR EMBL; X56129; CAA39594.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF03494; Beta-APP; 1.

DR PROSITE; PS00319; A4_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4_INTRA; PARTIAL.

DR Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).

FT NON_TER 58 58

FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

SQ

Query Match 68.4%; Score 39; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.81; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 2 VGSNKGAI 9

DB 29 VGSNKGAI 36

RESULT 5

ID A4_SHEEP STANDARD; PRT; 58 AA.

AC Q28757;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Caprinae; Ovis.

OC NCBI_TaxID=9940;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Heart;

RC MEDLINE=92017079; PubMed=1656157;

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

DR EMBL; X56124; CAA39589.1; -.

DR EMBL; X56126; CAA39591.1; -.

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CC -----

DR EMBL; X56130; CAA39595.1; -.

DR HSSP; P05067; 1BA4.

DR InterPro; IPR001868; A4_APP.

DR InterPro; IPR001255; Beta-APP.

DR Pfam; PF03494; Beta-APP; 1.

DR PROSITE; PS00319; A4_EXTRA; PARTIAL.

DR PROSITE; PS00320; A4_INTRA; PARTIAL.

DR Glycoprotein; Amyloid; Neurone; Transmembrane.

FT NON_TER 1 1

FT CHAIN 6 48 BETA-AMYLOID PROTEIN (POTENTIAL).

FT DOMAIN <1 33 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 34 57 POTENTIAL.

FT DOMAIN 58 >58 CYTOPLASMIC (POTENTIAL).

FT NON_TER 58 58

FT SEQUENCE 58 AA; 6300 MW; F434209D88EBA82D CRC64;

SQ

Query Match 68.4%; Score 39; DB 1; Length 58;
Best Local Similarity 100.0%; Pred. No. 0.81; Indels 0; Gaps 0;
Matches 8; Conservative 0; Mismatches 0;

QY 2 VGSNKGAI 9

DB 29 VGSNKGAI 36

RESULT 6

ID A4_BOVIN STANDARD; PRT; 59 AA.

AC Q28053;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DE Alzheimer's disease amyloid A4 protein homolog [Contains: Beta-amyloid protein (Beta-APP) (A-beta)] (Fragment).

GN APP.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

OX [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Brain;

RC MEDLINE=92017079; PubMed=1656157;

RX Johnstone E.M., Chaney M.O., Norris F.H., Pascual R., Little S.P.; "Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog, polar bear and five other mammals by cross-species polymerase chain reaction analysis.";

RT Brain Res. Mol. Brain Res. 10:299-305(1991).

RL Brain Res. Mol. Brain Res. 10:299-305(1991).

CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G(O) (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.

CC -----

DR EMBL; X56124; CAA39589.1; -.

DR EMBL; X56126; CAA39591.1; -.

```

DR HSP: P05067; IBA4.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF03494; Beta-APP.
DR PROSITE: PS00319; A4_EXTRA; PARTIAL.
DR PROSITE: PS00320; A4_INTRA; PARTIAL.
DR Glycoprotein: Amyloid; Neurone; Transmembrane.
FT NON_TER 1
FT CHAIN 7 49 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN <1 34 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 35 58 POTENTIAL.
FT DOMAIN 59 >59 CYTOPLASMIC (POTENTIAL).
FT NON_TER 59 59
FT SEQUENCE 59 AA; 6414 MW; F43469D48A2E12D CRC64;

Query Match 68.4%; Score 39; DB 1; Length 59;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9 PRT; 751 AA.
Db 30 VGSNKGAI 37

RESULT 7
ID A4_SAISC STANDARD; PRT; 751 AA.
AC Q95241;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP.
OS Saimiri sciureus (Common squirrel monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.
NCBI_TaxID=9521;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver, and Kidney;
RX MEDLINE=96108492; PubMed=8532114;
RA Levy E., Amorim A., Frangione B., Walker L.C.;
RT "Beta-amyloid precursor protein gene in squirrel monkeys with cerebral amyloid angiopathy."
RL Neurobiol. Aging 16:805-808(1995).
CC -!- FUNCTION: FUNCTIONAL NEURONAL RECEPTOR WHICH COUPLES TO INTRACELLULAR SIGNALING PATHWAY THROUGH THE GTP-BINDING PROTEIN G13.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF PHOSPHORYLATION (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
CC
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CC
CC ENBL: S81024; AAD14347.1; -.
DR HSP: P05067; IAAP.
DR InterPro: IPR001868; A4_APP.
DR InterPro: IPR001255; Beta-APP.
DR Pfam: PF00014; Kunitz_BPTI; 1.
DR Pfam: PF02177; A4_EXTRA; 1.

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DR Pfam: PF03494; Beta-APP; 1.
DR PRINTS: PR00203; AMYLOIDA4.
DR PRINTS: PR00759; BASICTASE.
DR PRODOM: PD000222; Kunitz_BPTI; 1.
DR SMART: SM00006; A4_EXTRA; 1.
DR SMART: SM00131; KU; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR PROSITE: PS00280; BPTI_KUNITZ_1; 1.
DR PROSITE: PS00279; BPTI_KUNITZ_2; 1.
DR Glycoprotein: Amyloid; Neurone; Transmembrane; Alternative splicing;
KW Signal; Serine protease inhibitor.
FT SIGNAL 1 17 BY SIMILARITY.
FT CHAIN 18 751 A4 PROTEIN.
FT CHAIN 653 695 BETA-AMYLOID PROTEIN (POTENTIAL).
FT DOMAIN 18 680 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 681 704 POTENTIAL.
FT DOMAIN 705 751 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
FT SITE 740 743 CLATHRIN-BINDING (BY SIMILARITY).
FT ACT_SITE 301 302 REACTIVE BOND.
FT DISULFID 291 341 BY SIMILARITY.
FT DISULFID 300 324 BY SIMILARITY.
FT DISULFID 316 337 BY SIMILARITY.
FT CARBOHYD 523 523 N-LINKED (GLCNAC. . .) (PROBABLE).
FT CARBOHYD 552 552 N-LINKED (GLCNAC. . .) (PROBABLE).
SQ SEQUENCE 751 AA; 84893 MW; 6C3E431089569049 CRC64;

Query Match 68.4%; Score 39; DB 1; Length 751;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 676 VGSNKGAI 683

RESULT 8
ID A4_HUMAN STANDARD; PRT; 770 AA.
AC P05067; P09000; Q16011;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Alzheimer's disease amyloid A4 protein precursor (Protease nexin-II) (PN-II) (APP) [Contains: Beta-amyloid protein (Beta-APP) (A-beta)].
GN APP OR A4 OR CVAP OR AD1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=87144572; PubMed=2881207;
RA Kang J., Lemaire H.-G., Unterbeck A., Salbaum J.M., Masters C.L., Grzeschik K.-H., Multhaup G., Beyreuther K., Mueller-Hill B.;
RT "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor."
RL Nature 325:733-736(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86122639; PubMed=2893289;
RA Ponce P., Gonzalez-Bewhitt P., Schilling J., Miller J., Hsu D., Greenberg B., Davis K., Wallace W., Lieberburg I., Fuller F., Cordell B.;
RT "A new A4 amyloid mRNA contains a domain homologous to serine proteinase inhibitors."
RL Nature 331:525-527(1988).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=89128427; PubMed=2783775;
RA Lemaire H.G., Salbaum J.M., Multhaup G., Kang J., Bayney R.M.,

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- RA Unterbeck A., Beyreuther K., Mueller-Hill B.;
RT "The PreA(695) precursor protein of Alzheimer's disease A4 amyloid
RT is encoded by 16 exons";
RL Nucleic Acids Res. 17:517-522(1989).
RN [4]
- RP SEQUENCE FROM N.A.
RX MEDLINE=97263807; PubMed=9108164;
RA Hattori M., Tsukahara F., Furuhashi Y., Tanahashi H., Hirose M.,
RA Saito M., Tsukuni S., Sakaki Y.;
RT "A novel method for making nested deletions and its application for
RT sequencing of a 300 kb region of human APP locus";
RL Nucleic Acids Res. 25:1802-1808(1997).
RN [5]
- RP SEQUENCE OF 286-345 AND 365-366 FROM N.A.
RX MEDLINE=88126640; PubMed=2893290;
RA Tanzi R.E., McClatchey A.I., Lamperti E.D., Villa-Komaroff L.,
RA Gusella J.F., Neve R.L.;
RT "Protease inhibitor domain encoded by an amyloid protein precursor
RT mRNA associated with Alzheimer's disease";
RL Nature 331:528-530(1988).
RN [6]
- RP SEQUENCE OF 287-367 FROM N.A.
RX MEDLINE=88126641; PubMed=2893291;
RA Kitaguchi N., Takahashi Y., Tokushima Y., Shiojiri S., Ito H.;
RT "Novel precursor of Alzheimer's disease amyloid protein shows
RT protease inhibitory activity";
RL Nature 331:530-532(1988).
RN [7]
- RP SEQUENCE OF 284-289 AND 365-770 FROM N.A.
RX MEDLINE=87231971; PubMed=3035574;
RA Robakis N.K., Ramakrishna N., Wolfe G., Wisniewski H.M.;
RT "Molecular cloning and characterization of a cDNA encoding the
RT cerebrovascular and the neuritic plaque amyloid peptides";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4190-4194(1987).
RN [8]
- RP "Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer
RT disease brain: coding and noncoding regions of the fetal precursor
RT mRNA are expressed in the cortex";
RL Proc. Natl. Acad. Sci. U.S.A. 85:929-933(1988).
RN [9]
- RP SEQUENCE OF 672-681.
RX MEDLINE=88035004; PubMed=3312495;
RA Pardridge W.M., Vinters H.V., Yang J., Eisenberg J., Choi T.B.,
RA Tourtelotte W.W., Huebner V., Shively J.E.;
RT "Amyloid angiopathy of Alzheimer's disease: amino acid composition
RT and partial sequence of a 4,200-dalton peptide isolated from cortical
RT microvessels";
RL J. Neurochem. 49:1394-1401(1987).
RN [10]
- RP SEQUENCE OF 739-770 FROM N.A.
RX MEDLINE=90236318; PubMed=2110105;
RA Yoshikawa S.-I., Sasaki H., Doh-Ura K., Furuya H., Sakaki Y.;
RT "Genomic organization of the human amyloid beta-protein precursor
RT gene";
RL Gene 87:257-263(1990).
RN [11]
- RP SEQUENCE OF 1-10 FROM N.A.
RX TISSUE=Liver;
RX MEDLINE=89016647; PubMed=3140222;
RA Schon E.A., Mita S., Sadlock J., Herbert J.;
RT "A cDNA specifying the human amyloid beta precursor protein (ABPP)
RT encodes a 95-kDa polypeptide";
RL Nucleic Acids Res. 16:9351-9351(1988).
RN [12]
- RP SEQUENCE OF 18-50.
RX MEDLINE=87250462; PubMed=3597385;
RA van Nostrand W.E., Cunningham D.D.;
RT "Purification of protease nexin II from human fibroblasts";
RL J. Biol. Chem. 262:8508-8514(1987).
RN [13]
- RP IDENTITY OF APP WITH NEXIN-II.
RX MEDLINE=89384866; PubMed=2506449;
RA Oltersdorf T., Fritz L.C., Schenk D.B., Lieberburg I.,
RA Johnson-Wood K.L., Beattie E.C., Ward P.J., Blacher R.W., Dovey H.F.,
RA Sinha S.;
RT "The secreted form of the Alzheimer's amyloid precursor protein with
RT the Kunitz domain is protease nexin-II";
RL Nature 341:144-147(1989).
RN [14]
- RP PROTEASE-SPECIFICITY OF INHIBITOR DOMAIN.
RX MEDLINE=90211252; PubMed=1969731;
RA Kido H., Fukutomi A., Schilling J., Wang Y., Cordell B., Katunuma N.;
RT "Protease-specificity of Kunitz inhibitor domain of Alzheimer's
RT disease amyloid protein precursor";
RL Biochem. Biophys. Res. Commun. 167:716-721(1990).
RN [15]
- RP COMPLEX WITH G(O).
RX MEDLINE=93188965; PubMed=8446172;
RA Nishimoto I., Okamoto T., Matsuura Y., Takahashi S., Okamoto T.,
RA Murayama Y., Ogata E.;
RT "Alzheimer amyloid protein precursor complexes with brain GTP-binding
RT protein G(O)";
RL Nature 362:75-79(1993).
RN [16]
- RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 28-133.
RX MEDLINE=99215582; PubMed=10201399;
RA Rossjohn J., Cappai R., Feil S.C., Henry A., McKinstry W.J.,
RA Galatis D., Hesse L., Multhaup G., Beyreuther K., Masters C.L.,
RA Parker M.W.;
RT "Crystal structure of the N-terminal, growth factor-like domain of
RT Alzheimer amyloid precursor protein";
RL Nat. Struct. Biol. 6:327-331(1999).
RN [17]
- RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS) OF 287-344.
RX MEDLINE=91104913; PubMed=2125487;
RA Hynes T.R., Randall M., Kennedy L.A., Eigenbrot C., Kossiakof A.A.;
RT "X-ray crystal structure of the protease inhibitor domain of
RT Alzheimer's amyloid beta-protein precursor";
RL Biochemistry 29:10018-10022(1990).
RN [18]
- RP STRUCTURE BY NMR OF 289-344.
RX MEDLINE=92031488; PubMed=1718421;
RA Heald S.L., Tilton R.F. Jr., Hammond L.S., Lee A., Bayney R.M.,
RA Kamark M.E., Ramabhadran T.V., Dreyer R.N., Davis G., Unterbeck A.,
RA Tamburini P.P.;
RT "Sequential NMR resonance assignment and structure determination of
RT the Kunitz-type inhibitor domain of the Alzheimer's beta-amyloid
RT precursor protein";
RL Biochemistry 30:10467-10478(1991).
RN [19]
- RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=94281210; PubMed=7516706;
RA Talafous J., Marcinkowski K.J., Klopman G., Zagorski M.G.;
RT "Solution structure of residues 1-28 of the amyloid beta-peptide";
RL Biochemistry 33:7788-7796(1994).
RN [20]
- RP STRUCTURE BY NMR OF 696-706.
RX MEDLINE=97128622; PubMed=8973180;
RA Kohno T., Kobayashi K., Maeda T., Sato K., Takashima A.;
RT "Three-dimensional structures of the amyloid beta peptide (25-35) in
RT membrane-mimicking environment";
RL Biochemistry 35:16094-16104(1996).
RN [21]
- RP STRUCTURE BY NMR OF 672-711.
RX MEDLINE=98359783; PubMed=9693002;
RA Coles M., Bicknell W., Watson A.A., Fairlie D.P., Craik D.J.;
RT "Solution structure of amyloid beta-peptide(1-40) in a water-micelle
RT environment. Is the membrane-spanning domain where we think it is?";
RL Biochemistry 37:11064-11077(1998).
RN [22]
- RP STRUCTURE BY NMR OF 672-699.
RX MEDLINE=20400066; PubMed=10940222;

RA Poulsen S.A., Watson A.A., Craik D.J.;
 RT "Solution structures in aqueous SDS micelles of two amyloid beta
 RT peptides of Abeta(1-28) mutated at the alpha-secretase cleavage
 RT site.";
 RL J. Struct. Biol. 130:142-152(2000).
 RN [23]
 RP STRUCTURE BY NMR OF 681-706.
 RX MEDLINE=20400065; PubMed=10940221;
 RA Zhang S., Iwata K., Lachenmann M.J., Peng J.W., Li S., Stimson E.R.,
 RA Lu Y., Felix A.M., Maggio J.E., Lee J.P.;
 RT "The Alzheimer's peptide a beta adopts a collapsed coil structure in
 RT water.";
 RL J. Struct. Biol. 130:130-141(2000).
 RN [24]
 RP SIGNAL SEQUENCE CLEAVAGE SITE, AND TOPOLOGY.
 RX MEDLINE=88296437; PubMed=2900137;
 RA Dykx T., Weidemann A., Multhaup G., Salbaum J.M., Lemaire H.-G.,
 RA Kang J., Mueller-Hill B., Masters C.L., Beyreuther K.;
 RT "Identification, transmembrane orientation and biogenesis of the
 RT amyloid A4 precursor of Alzheimer's disease.";
 Query Match 68.4%; Score 39; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VGSNKGAI 9
 Db 695 VGSNKGAI 702
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 RESULT 9
 A4_MOUSE STANDARD; PRT: 770 AA.
 ID A4_MOUSE
 AC P12023;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=92096458; PubMed=1756177;
 RA de Strooper B., van Leuven F., van den Berghe H.;
 RT "The amyloid beta protein precursor or proteinase nexin II from mouse
 RT is closer related to its human homolog than previously reported.";
 RL Biochim. Biophys. Acta 1129:141-143(1991).
 RN [2]
 RP SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88108489; PubMed=3322280;
 RA Yamada T., Sasaki H., Furuya H., Miyata T., Goto I., Sasaki Y.;
 RT "Complementary DNA for the mouse homolog of the human amyloid beta
 RT protein precursor.";
 RL Biochem. Biophys. Res. Commun. 149:665-671(1987).
 RN [3]
 RP REVISTONS.
 RA Yamada T.;
 RL Submitted (MAR-1988) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC STRAIN=CD-1; TISSUE=Placenta;
 RX MEDLINE=89345111; PubMed=2569710;
 RA Fukuchi K., Martin G.M., Deeb S.S.;
 RT "Sequence of the protease inhibitor domain of the A4 amyloid protein
 RT precursor of Mus domesticus";
 RL Nucleic Acids Res. 17:5396-5396(1989).
 RN [5]

RP SEQUENCE OF 1-19 FROM N.A.
 RX MEDLINE=92209998; PubMed=1555768;
 RA Izumi R., Yamada T., Yoshikai S.I., Sasaki H., Hattori M.,
 RA Sakai Y.;
 RT "Positive and negative regulatory elements for the expression of the
 RT Alzheimer's disease amyloid precursor-encoding gene in mouse.";
 RL Gene 112:189-195(1992).
 RN [6]
 RP SEQUENCE OF 281-380 FROM N.A., AND ALTERNATIVE SPLICING.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=89149813; PubMed=2493250;
 RA Yamada T., Sasaki H., Dohura K., Goto I., Sasaki Y.;
 RT "Structure and expression of the alternatively-spliced forms of mRNA
 RT for the mouse homolog of Alzheimer's disease amyloid beta protein
 RT precursor.";
 RL Biochem. Biophys. Res. Commun. 158:906-912(1989).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: AAA(770) IS EXPRESSED IN KIDNEY. AAA(751) IS
 CC WIDELY EXPRESSED. AAA(695) IS EXPRESSED IN BRAIN, KIDNEY AND
 CC LIVER.
 CC -1- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC -----
 DR EMBL; X59379; ; NOT_ANNOTATED_CDS.
 DR EMBL; M18373; AAA37139.1; -
 DR EMBL; X15210; CAA33280.1; -
 DR EMBL; D10603; BAA01456.1; -
 DR EMBL; M24397; AAA39929.1; -
 DR PIR; A27485; A27485.
 DR PIR; S04855; S04855.
 DR PIR; S19727; S19727.
 DR HSP; P05067; 1AAP.
 DR MGD; MGI:88059; App.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS0279; BPTI_KUNITZ_2; 1.
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 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17
 FT CHAIN 18 770
 FT ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT DOMAIN 18 699
 FT EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723
 FT POTENTIAL.
 FT DOMAIN 724 770
 FT CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 673 715
 FT EQUIVALENT OF BETA-AMYLOID PROTEIN.

FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
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 FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 289 289 E -> V (IN ISOFORM APP(695)).
 FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).
 FT VARSPLIC 346 380 MISSING (IN ISOFORM APP(751)).
 SQ SEQUENCE 770 AA; 86752 MW; 26C50DE0890CAFA7A CRC64;

Query Match 68.4%; Score 39; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 |||||

Db 695 VGSNKGAI 702

RESULT 10

A4_RAT
 ID A4_RAT STANDARD; PRT; 770 AA.
 AC P08592;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Alzheimer's disease amyloid A4 protein homolog precursor
 DE (Amyloidogenic glycoprotein) (AG).
 GN APP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 [1]
 RN SEQUENCE OF 1-289 AND 365-770 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=88312583; PubMed=2900758;
 RA Shivers B.D., Hilbich C., Multhaup G., Salbaum J.M., Beyreuther K.,
 RA Seeburg P.H.;
 RT "Alzheimer's disease amyloidogenic glycoprotein: expression pattern
 in rat brain suggests a role in cell contact.";
 RL EMBO J. 7:1365-1370(1988).
 RN [2]
 RP SEQUENCE OF 289-364 FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=89183625; PubMed=2648331;
 RA Kang J., Mueller-Hill B.;
 RT "The sequence of the two extra exons in rat preA4.";
 RL Nucleic Acids Res. 17:2130-2130(1989).
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; APP(395), APP(563), APP(695),
 CC APP(751) AND APP(770) (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -!- DOMAIN: THE CLATHRIN-BINDING SITE IS ESSENTIAL FOR ITS ASSOCIATION
 CC WITH X11-ALPHA, -BETA, AND -GAMMA. THE SEQUENCE SPECIFIC
 CC RECOGNITION EXTENDS TO PEPTIDE RESIDUES THAT ARE C-TERMINAL TO THE
 CC NPXY MOTIF. THIS INTERACTION APPEARS TO BE INDEPENDENT OF
 CC PHOSPHORYLATION (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE APP FAMILY.
 CC -!- SIMILARITY: CONTAINS 1 BPTI/KUNITZ INHIBITOR DOMAIN.
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 CC
 CC EMBL; X07648; CAA30488.1; -;
 CC EMBL; X14066; CAA32229.1; -;

DR PIR; S00550; S00550.
 DR PIR; S03607; S03607.
 DR HSP; P05067; IAAP.
 DR InterPro; IPR001868; A4_APP.
 DR InterPro; IPR001255; Beta_APP.
 DR InterPro; IPR002223; Kunitz_BPTI.
 DR Pfam; PF00014; Kunitz_BPTI; 1.
 DR Pfam; PF02177; A4_EXTRA; 1.
 DR Pfam; PF03494; Beta_APP; 1.
 DR PRINTS; PR00203; AMYLOIDA4.
 DR PRINTS; PR00759; BASICPTASE.
 DR ProDom; PD000222; Kunitz_BPTI; 1.
 DR SMART; SM00006; A4_EXTRA; 1.
 DR SMART; SM00131; KU; 1.
 DR PROSITE; PS00319; A4_EXTRA; 1.
 DR PROSITE; PS00320; A4_INTRA; 1.
 DR PROSITE; PS00280; BPTI_KUNITZ_1; 1.
 DR PROSITE; PS00279; BPTI_KUNITZ_2; 1.
 DR KW Glycoprotein; Amyloid; Neurone; Transmembrane; Signal;
 KW Alternative splicing; Serine protease inhibitor.
 FT SIGNAL 1 17 BY SIMILARITY.
 FT CHAIN 18 770 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN
 FT HOMOLOG.
 FT DOMAIN 18 699 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 700 723 POTENTIAL.
 FT DOMAIN 724 770 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 673 715 EQUIVALENT OF BETA-AMYLOID PROTEIN.
 FT DOMAIN 287 345 BPTI/KUNITZ INHIBITOR.
 FT SITE 759 762 CLATHRIN-BINDING (BY SIMILARITY).
 FT DISULFID 291 341 BY SIMILARITY.
 FT DISULFID 300 324 BY SIMILARITY.
 FT DISULFID 316 337 BY SIMILARITY.
 FT CARBOHYD 542 542 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 571 571 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 289 289 E -> V (IN ISOFORM APP(695)).
 FT VARSPLIC 290 364 MISSING (IN ISOFORM APP(695)).
 SQ SEQUENCE 770 AA; 86704 MW; C26C9D6B8D929A7 CRC84;

Query Match 68.4%; Score 39; DB 1; Length 770;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VGSNKGAI 9
 |||||

Db 695 VGSNKGAI 702

RESULT 11

ADEC_ARCFU
 ID ADEC_ARCFU STANDARD; PRT; 556 AA.
 AC O29999;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable adenine deaminase (EC 3.5.4.2) (Adenase) (Adenine aminase).
 GN AFO240.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales;
 OC Archaeoglobaceae; Archaeoglobus.
 OC NCBI_TaxID=2234;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE=98049343; PubMed=9389475;
 RA Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
 RA Ketchum K.A., Dodson R.J., Winn M., Hickey E.K., Peterson J.D.,
 RA Richardson D.L., Kierlavage A.R., Graham D.E., Kyprides N.C.,
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,
 RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
 RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
 RA Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M.,
 RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,

RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
 RA Venter J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 reducing archaeon *Archaeoglobus fulgidus*.";
 RL Nature 390:364-370(1997).
 CC -1- CATALYTIC ACTIVITY: Adenine + H(2)O = hypoxanthine + NH(3).
 CC -1- SIMILARITY: BELONGS TO THE ADENINE DEAMINASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AE001089; AAB90993.1; -
 DR TIGR; AF0240; -
 DR InterPro; IPR002832; Adenine_deam.
 DR Pfam; PF01979; Adenine_deam; 1.
 DR TIGRFAMs; TIGR01178; ade; 1.
 KW Hypothetical protein; Hydrolase; Complete proteome.
 SQ SEQUENCE 556 AA; 60764 MW; B3E3440A09F86A79 CRC64;

 Query Match 64.9%; Score 37; DB 1; Length 556;
 Best Local Similarity 60.0%; Pred. No. 16;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CVGSNKGATC 10
 ||| | :|||
 DB 450 CVGVDDGSGIC 459

 RESULT 12
 PURI_METH STANDARD; PRT; 474 AA.
 ID PURI_METH
 AC O26742;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Amidophosphoribosyltransferase precursor (EC 2.4.2.14) (Glutamine
 DE phosphoribosylpyrophosphate amidotransferase) (ATASE) (GPATase).
 GN PURF OR MTH646.
 OS Methanobacterium thermoautotrophicum.
 OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
 OC Methanobacteriaceae; Methanothermobacter.
 OX NCBI_TaxID=187420;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Delta H;
 RX MEDLINE=98037514; PubMed=9371463;
 RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
 RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
 RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
 RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
 RA Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
 RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
 RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
 RA "Complete genome sequence of Methanobacterium thermoautotrophicum
 RA deltaH: functional analysis and comparative genomics.";
 RL J. Bacteriol. 179:7135-7155(1997).
 CC -1- CATALYTIC ACTIVITY: 5-phospho-beta-D-ribose + diphosphate +
 CC L-glutamate = L-glutamine + 5-phospho-alpha-D-ribose 1-diphosphate
 CC + H(2)O.
 CC -1- PATHWAY: De novo purine biosynthesis; first step.
 CC -1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE
 CC PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AE000845; AAB85151.1; -
 DR HSP; P00497; IAGO.
 DR InterPro; IPR000583; GATase_2.
 DR InterPro; IPR000836; PRTtransferase.
 DR Pfam; PF002375; Pr/PY_rp.transf.
 DR Pfam; PF00156; Pribosyltran; 1.
 DR Pfam; PF00310; GATase_2; 1.
 DR TIGRFAMs; TIGR01134; purF; 1.
 DR PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
 DR PROSITE; PS00443; GATASE_TYPE_II; 1.
 KW Purine biosynthesis; Transferase; Glycosyltransferase;
 KW Glutamine amidotransferase; Complete proteome.
 FT PROPEP 1 10
 FT CHAIN 11 474
 FT ACT_SITE 11 474
 FT ACT_SITE 11 474
 SQ SEQUENCE 474 AA; 52660 MW; 16BAF93BBF15A0D2 CRC64;

 Query Match 63.2%; Score 36; DB 1; Length 474;
 Best Local Similarity 50.0%; Pred. No. 22;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CVGSNKGATC 10
 ||| | :|||
 DB 438 CIGIKKGFLC 447

 RESULT 13
 KLB8_HUMAN STANDARD; PRT; 260 AA.
 ID KLB8_HUMAN
 AC O60259; Q9UQ47; Q9HCB3; Q9UIL9;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neuropilin precursor (EC 3.4.21.-) (NP) (kallikrein 8) (Ovasin) (Serine
 DE protease TAGD-14) (Tumor-associated differentially expressed gene-14
 DE protein).
 GN KLB8 OR PRSS19 OR TAGD14 OR NRPN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Hippocampus;
 RX MEDLINE=98372070; PubMed=9714609;
 RA Yoshida S., Taniguchi M., Hirata A., Shiosaka S.;
 RT "Sequence analysis and expression of human neuropsin cDNA and gene.";
 RL Gene 213:9-16(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=98203457; PubMed=10102990;
 RA Mitsui S., Tsuruoka N., Yamashiro K., Nakazato H., Yamaguchi N.;
 RT "A novel form of human neuropsin, a brain-related serine protease, is
 RT generated by alternative splicing and is expressed preferentially in
 RT human adult brain.";
 RL Eur. J. Biochem. 260:627-634(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Ovary;
 RX MEDLINE=99413504; PubMed=10485494;
 RA Underwood L.J., Tanimoto H., Wang Y., Shigemasa K., Parmley T.H.,
 RA O'Brien T.J.;
 RT "Cloning of tumor-associated differentially expressed gene-14, a novel
 RT serine protease overexpressed by ovarian carcinoma.";
 RL Cancer Res. 59:4435-4439(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Gan L., Gelinis R., Gown A.M., Moss P., Smith R., Wang K.;

"Molecular cloning and characterization of a novel serine protease, ovastin, a potential molecular marker for ovarian carcinomas.";
Submitted (SFP-1998) to the EMBL/GenBank/DBJ databases.

[5]

SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=20510030; PubMed=11054574;

Gan L., Lee I., Smith R., Argonza-Barrett R., Lei H., McCuaig J.,

Moss P., Paepel B., Wang K.;

"Sequencing and expression analysis of the serine protease gene

cluster located in chromosome 19q13 region.";

Gene 257:119-130(2000).

[6]

SEQUENCE OF 1-164 FROM N.A. (ISOFORM 1).

Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,

Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,

Phan H., Velasco N., Do L., Regala W., Terry A., Brower A., Garnes J.,

Dangnan L., Eriar A., Christensen M., Amico-Keller G., Coefield J.,

Duarte S., Lucas S., Bruce R., Attix C., Amico-Keller G., Coefield J.,

Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A.,

Olsen A.S., Carrano A.V.;

"Sequence analysis of chromosome 19q13.4.";

Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.

[6]

-!- FUNCTION: SUGGESTED TO BE INVOLVED IN KINDLING EPILEPTOGENESIS AND

HIPPOCAMPAL PLASTICITY.

-!- CATALYTIC ACTIVITY: PREFERENTIAL CLEAVAGE: ARG-, LYS-.

-!- SUBCELLULAR LOCATION: Secreted.

-!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE

PRODUCED BY ALTERNATIVE SPLICING.

-!- TISSUE SPECIFICITY: ISOFORM 1 IS PREDOMINANTLY EXPRESSED IN THE

PANCREAS WHILE ISOFORM 2 IS EXPRESSED IN ADULT BRAIN AND

HIPPOCAMPUS. BOTH FORMS ARE ALSO FOUND IN FETAL BRAIN AND

PLACENTA. NOT DETECTED IN KIDNEY, SPLEEN, LIVER AND LUNG.

-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1. KALLIKREIN SUBFAMILY.

[1]

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[1]

EMBL; AB009849; BAA28673.1; -

EMBL; AB012761; BAA28676.1; -

EMBL; AB010780; BAA88684.1; -

EMBL; AB008390; BAA82665.1; -

EMBL; AB008927; BAA82666.1; -

EMBL; AF055982; AAD56050.1; -

EMBL; AF095742; AAD25979.1; -

EMBL; AF095743; AAD25974.1; -

EMBL; AF243527; AAG33361.1; -

EMBL; AC011473; AAG23254.1; -

HSP; O61955; INPM.

MEROPS; S01.244; -

Genew; HGNC:6369; KLR8.

MIM; 605644; -

InterPro: IPR001314; Chymotrypsin.

InterPro: IPR001254; Ser.protease_Try.

Pfam: PF00089; trypsin; 1.

PRINTS; PR00722; CHYMOTRYPSIN.

SMART; SM00020; Tryp_Spc; 1.

PROSITE; PS02040; TRYPSIN_DOM; 1.

PROSITE; PS00134; TRYPSIN_HIS; 1.

PROSITE; PS00135; TRYPSIN_SER; 1.

Hydrolase; Serine protease; Glycoprotein; Zymogen; Signal;

KW

Alternative splicing.

SIGNAL 1 28 POTENTIAL.

PROPEP 29 32 BY SIMILARITY.

CHAIN 33 260 NEUROPSIN.

ACT_SITE 73 73 CHARGE RELAY SYSTEM (BY SIMILARITY).

ACT_SITE 120 120 CHARGE RELAY SYSTEM (BY SIMILARITY).

ACT_SITE 212 212 CHARGE RELAY SYSTEM (BY SIMILARITY).

FT

FT DISULFID 39 173 BY SIMILARITY.
FT DISULFID 58 74 BY SIMILARITY.
FT DISULFID 145 246 BY SIMILARITY.
FT DISULFID 152 218 BY SIMILARITY.
FT DISULFID 184 198 BY SIMILARITY.
FT DISULFID 208 233 BY SIMILARITY.
FT CARBOHYD 110 110 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 23 23 WRSNPLPPAA (IN ISOFORM 2).
SQ SEQUENCE 260 AA; 28048 MW; EF439E5B8C8E660 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 260;
Best Local Similarity 75.0%; Pred. No. 19;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGK 8
Db 198 CAGSSKGA 205
| 11:11111

RESULT 14

FP2_MVTGA STANDARD; PRT; 473 AA.
ID FP2_MVTGA STANDARD; PRT; 473 AA.
AC 025464;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Adhesive plaque matrix protein 2 precursor (Foot protein 2) (MGFP2)
DE (MGFP-2).
GN FP2.
OS Mytilus galloprovincialis (Mediterranean mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=291158;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Foot.
RA MEDLINE=95204464; PubMed=7896812;
RX Inoue K., Takeuchi Y., Miki D., Odo S.;
RT "Mussel adhesive plaque protein gene is a novel member of epidermal
growth factor-like gene family.";
RL J. Biol. Chem. 270:6698-6701(1995).
CC -!- FUNCTION: PROVIDES ADHESIVENESS TO THE MUSSEL'S FOOT. MUSSELS
PRODUCE ONE OF THE STRONGEST WATER INSOLUBLE GLUE. THE MUSSEL'S
ADHESIVE IS A BUNDLE OF THREADS, CALLED A BYSSUS, FORMED BY A
FIBROUS COLLAGENOUS CORE COATED WITH ADHESIVE PROTEINS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: PRODUCED BY THE BYSSAL GLAND.
CC -!- DEVELOPMENTAL STAGE: EXPRESSION STARTS AT THE PEDIVELIGER, FOOT
FORMATION, STAGE.
CC -!- PTM: SOME TYROSINES ARE HYDROXYLATED (THUS PRODUCING DOPA - 3,4-
DIHYDROXYPHENYLALANINE).
CC -!- SIMILARITY: CONTAINS 11 EGF-LIKE DOMAINS.
CC -----
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EMBL; D43794; BAA07852.1; -

HSSP; P00740; IEDM.

InterPro: IPR000152; Asx_hydroxyl.

InterPro: IPR000561; EGF-like.

InterPro: IPR000742; EGF-2.

InterPro: IPR001881; EGF_Ca.

Pfam; PF00008; EGF; 11.

SMART; SM00181; EGF; 10.

PROSITE; PS00010; ASX_HYDROXYL; 2.

PROSITE; PS00022; EGF_1; 11.

PROSITE; PS01186; EGF_2; 10.

KW Glycoprotein; EGF-like domain; Repeat; Signal; Hydroxylation.
 FT SIGNAL 1 17
 FT CHAIN 18 473
 FT DOMAIN 45 81
 FT DOMAIN 82 117
 FT DOMAIN 118 154
 FT DOMAIN 155 191
 FT DOMAIN 192 228
 FT DOMAIN 229 265
 FT DOMAIN 266 301
 FT DOMAIN 302 340
 FT DOMAIN 342 378
 FT DOMAIN 383 420
 FT DOMAIN 425 461
 FT MOD_RES 23 23
 FT MOD_RES 31 31
 FT MOD_RES 36 36
 FT MOD_RES 43 43
 FT CARBOHYD 93 93
 FT DISULFID 49 60
 FT DISULFID 54 69
 FT DISULFID 71 80
 FT DISULFID 86 97
 FT DISULFID 91 106
 FT DISULFID 108 117
 FT DISULFID 122 133
 FT DISULFID 127 143
 FT DISULFID 145 154
 FT DISULFID 159 170
 FT DISULFID 164 180
 FT DISULFID 182 191
 FT DISULFID 196 207
 FT DISULFID 201 217
 FT DISULFID 219 228
 FT DISULFID 233 244
 FT DISULFID 238 254
 FT DISULFID 256 265
 FT DISULFID 270 281
 FT DISULFID 275 290
 FT DISULFID 292 301
 FT DISULFID 306 317
 FT DISULFID 311 328
 FT DISULFID 330 339
 FT DISULFID 346 357
 FT DISULFID 351 366
 FT DISULFID 368 377
 FT DISULFID 387 399
 FT DISULFID 393 408
 FT DISULFID 410 419
 FT DISULFID 429 440
 FT DISULFID 434 449
 FT DISULFID 451 460
 SQ SEQUENCE 473 AA; 51772 MW; BA76BA8C3BA49A0F CRC64;

Query Match 61.4%; Score 35; DB 1; Length 473;
 Best Local Similarity 60.0%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CVGSKNGAIC 10
 III II I
 Db 330 CVGSKNGAIC 339

RESULT 15

TAL_HELPJ STANDARD; PRT; 316 AA.
 ID TAL_HELPJ
 AC G9ZJCS;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Transaldolase (EC 2.2.1.2).
 GN TAL OR JHP1388.
 OS Helicobacter pylori J99 (Campylobacter pylori J99).

OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
 OC Helicobacter.
 OX NCBI_TaxID=85963;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99120557; PubMed=9923682;
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
 Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
 Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
 Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
 Trust T.J.;
 RT "Genomic sequence comparison of two unrelated isolates of the human
 gastric pathogen Helicobacter pylori";
 RL Nature 397:176-180(1999).
 CC -!- FUNCTION: Transaldolase is important for the balance of
 metabolites in the pentose-phosphate pathway (By similarity).
 CC -!- CATALYTIC ACTIVITY: Sedoheptulose 7-phosphate + D-glyceraldehyde
 3-phosphate = D-erythrose 4-phosphate + D-fructose 6-phosphate.
 CC -!- PATHWAY: Pentose phosphate pathway; nonoxidative part.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
 CC -!- SIMILARITY: BELONGS TO THE TRANSALDOLASE FAMILY. SUBFAMILY 2.
 CC -----
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 CC -----
 DR EMBL; AE001561; AAD06969.1; -
 DR InterPro; IPR004732; Tal_mycobact.
 DR InterPro; IPR001585; Transaldolase.
 DR Pfam; PF00923; Transaldolase; 1.
 DR TIGRfams; TIGR00876; tal_mycobact; 1.
 DR PROSITE; PS01054; TRANSALDOLASE_1; 1.
 DR PROSITE; PS00958; TRANSALDOLASE_2; FALSE NEG.
 KW Transferase; Pentose shunt; Complete proteome.
 FT ACT_SITE 127 127 BY SIMILARITY.
 SQ SEQUENCE 316 AA; 35340 MW; 36D527596C96341B CRC64;
 Query Match 59.6%; Score 34; DB 1; Length 316;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 NKGATC 10
 IIIII
 Db 25 NKGATC 30

Search completed: November 9, 2002, 14:01:43
 Job time : 8.69231 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:34 ; Search time 13.8462 Seconds
(without alignments)
69.430 Million cell updates/sec

Title: US-09-632-748-4

Perfect score: 57

Sequence: 1 CVGSNKGGAIC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	70.2	284	2	F82666
2	39	68.4	42	2	PN0512
3	39	68.4	57	2	E60045
4	39	68.4	57	2	F60045
5	39	68.4	57	2	G60045
6	39	68.4	57	2	D60045
7	39	68.4	57	2	A60045
8	39	68.4	57	2	B60045
9	39	68.4	82	2	P00438
10	39	68.4	695	1	A49795
11	39	68.4	695	2	A27485
12	39	68.4	695	2	S00550
13	39	68.4	747	2	QH0773
14	39	68.4	770	2	Q8H044
15	38	66.9	372	2	T29359
16	37	64.9	89	2	T22622
17	37	64.9	556	2	H69279
18	36	63.2	474	2	H69185
19	36	63.2	1088	2	A69493
20	36	63.2	1555	2	T18688
21	36	63.2	1973	2	G89608
22	36	63.2	1973	2	T18686
23	35	61.4	299	2	F95294
24	35	61.4	473	2	A56175
25	35	61.4	786	2	H69980
26	34	59.6	87	2	A38725
27	34	59.6	191	2	T19573
28	34	59.6	191	2	T22036
29	34	59.6	316	2	G64706

30	34	59.6	316	2	E71812
31	34	59.6	356	2	T22998
32	34	59.6	426	2	T51506
33	34	59.6	457	1	G70116
34	34	59.6	470	2	T45816
35	34	59.6	611	2	S76211
36	34	59.6	615	2	T20839
37	34	59.6	640	2	T19346
38	34	59.6	644	2	B71409
39	34	59.6	661	1	A42287
40	34	59.6	661	2	T42754
41	34	59.6	752	2	AD2076
42	34	59.6	795	2	T52516
43	34	59.6	797	2	S28103
44	34	59.6	1391	2	T20406
45	34	59.6	1628	2	T43682

ALIGNMENTS

RESULT 1

F82666

Phage-related protein XP1555 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: F82666

R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: AB2515; MUID:20365717; PMID:10910347

A;Note: for a complete list of authors see reference number A59328 below

A;Accession: F82666

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1284 <SIM>

A;Cross-references: GB:AE003985; GB:AE0039849; NID:g9106593; PIDN:AAF84364.1; GSPDB:GN

A;Experimental source: strain 9a5c

R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer

as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Praga, J.S.; Franca, S.C.; Franco, M.C.; Fr

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuranae, E.E.; La

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins

A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa

A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silv

M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.

A;Reference number: A59328

A;Contents: annotation

C;Genetics:

A;Gene: XP1555

Query Match

Best Local Similarity 70.2%; Score 40; DB 2; Length 284;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CVGSNKGGAIC 10

Db 248 CVGDDGALC 257

RESULT 2

PN0512

Beta-amyloid protein - guinea pig (fragment)

C;Species: Cavia porcellus (guinea pig)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C;Accession: PN0512

R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.; Ohno

Biochem. Biophys. Res. Commun. 193, 624-630, 1993

A;Title: Receptor-mediated specific biological activity of a beta-amyloid protein fra

A:Reference number: PN0512; MUID:93290653; PMID:7685598
A:Accession: PN0512
A:Molecule type: protein
A:Residues: 1-42 <SHT>
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; amyloid

Query Match 68.4%; Score 39; DB 2; Length 42;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
|||||||
DB 24 VGSNKGAI 31

RESULT 3

E60045
Alzheimer's disease amyloid beta/A4 protein precursor - sheep (fragment)
C:Species: Ovis sp. (sheep)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: E60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: E60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56130
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
|||||||
DB 29 VGSNKGAI 36

RESULT 4

F60045
Alzheimer's disease amyloid beta/A4 protein precursor - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
C:Accession: F60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: F60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56127; NID:gl895; PIDN:CAA9592.1; PID:gl896
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
|||||||
DB 29 VGSNKGAI 36

RESULT 5

G60045
Alzheimer's disease amyloid beta/A4 protein precursor - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995

C:Accession: G60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: G60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56126
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
|||||||
DB 29 VGSNKGAI 36

RESULT 6

D60045
Alzheimer's disease amyloid beta/A4 protein precursor - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: D60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: D60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56124
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
|||||||
DB 29 VGSNKGAI 36

RESULT 7

A60045
Alzheimer's disease amyloid beta/A4 protein precursor - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 28-Jul-1995
C:Accession: A60045
R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
Brain Res. Mol. Brain Res. 10, 299-305, 1991
A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in d
A:Reference number: A60045; MUID:92017079; PMID:1656157
A:Accession: A60045
A:Molecule type: mRNA
A:Residues: 1-57 <JOH>
A:Cross-references: EMBL:X56125
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
|||||||
DB 29 VGSNKGAI 36

RESULT 8

B60045
 Alzheimer's disease amyloid beta/A4 protein precursor - polar bear (fragment)
 C:Species: Ursus maritimus (polar bear)
 C:Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 13-Aug-1999
 C:Accession: B60045
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: B60045
 A:Molecule type: mRNA
 A:Residues: 1-57 <JOH>
 A:Cross-references: EMBL:X56128; NID:92165; PIDN:CAA9593.1; PID:92166
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; brain

Query Match 68.4%; Score 39; DB 2; Length 57;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VGSNKGAI 9
 |||||
 DB 29 VGSNKGAI 36

RESULT 9

PQ0438
 Alzheimer's disease amyloid A4 protein precursor - rabbit (fragment)
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 30-Sep-1993 #sequence_revision 19-Oct-1995 #text_change 19-Oct-1995
 C:Accession: PQ0438; C60045
 R:Davidson, J.S.; West, R.L.; Kotikalapudi, P.; Maroun, L.E.
 Biochem. Biophys. Res. Commun. 188, 905-911, 1992
 A:Title: Sequence and methylation in the beta/A4 region of the rabbit amyloid precursor
 A:Reference number: PQ0438; MUID:93075180; PMID:1445331
 A:Accession: PQ0438
 A:Molecule type: DNA
 A:Residues: 1-82 <DAV>
 A:Cross-references: GB:M83558; GB:M83657
 R:Johnstone, E.M.; Chaney, M.O.; Norris, F.H.; Pascual, R.; Little, S.P.
 Brain Res. Mol. Brain Res. 10, 299-305, 1991
 A:Title: Conservation of the sequence of the Alzheimer's disease amyloid peptide in dog,
 A:Reference number: A60045; MUID:92017079; PMID:1656157
 A:Accession: C60045
 A:Molecule type: mRNA
 A:Residues: 12-68 <JOH>
 A:Cross-references: EMBL:X56129
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; Alzheimer's disease; amyloid; Down's syndrome

Query Match 68.4%; Score 39; DB 2; Length 82;
 Best Local Similarity 100.0%; Pred. No. 3.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 VGSNKGAI 9
 |||||
 DB 40 VGSNKGAI 47

RESULT 10

A49795
 Alzheimer's disease amyloid beta protein precursor - crab-eating macaque
 C:Species: Macaca fascicularis (crab-eating macaque)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A49795
 R:Podlisky, M.B.; Tolan, D.R.; Selkoe, D.J.
 Am. J. Pathol. 138, 1423-1435, 1991
 A:Title: Homology of the amyloid beta protein precursor in monkey and human supports a
 A:Reference number: A49795; MUID:91273117; PMID:1905108
 A:Accession: A49795
 A>Status: preliminary
 A:Molecule type: mRNA

A:Residues: 1-695 <POD>

A:Cross-references: GB:M58727; NID:g342062; PIDN:AAA36829.1; PID:g342063
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing

Query Match 68.4%; Score 39; DB 1; Length 695;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 |||||
 DB 620 VGSNKGAI 627

RESULT 11

A27485
 Alzheimer's disease amyloid beta/A4 protein homolog precursor - mouse
 N:Alternate names: proteinase nexin II
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 13-Aug-1999
 C:Accession: A27485; S19727; I49485
 R:Yamada, T.; Sasaki, H.; Furuya, H.; Miyata, T.; Goto, I.; Sakaki, Y.
 Biochem. Biophys. Res. Commun. 149, 665-671, 1987
 A:Title: Complementary DNA for the mouse homolog of the human amyloid beta protein pr
 A:Reference number: A27485; MUID:88106489; PMID:3322280
 A:Accession: A27485
 A:Molecule type: mRNA
 A:Residues: 1-695 <YAM>

A:Cross-references: GB:M18373; NID:g191568; PIDN:AAA37139.1; PID:g309085
 A:Experimental source: brain
 R:de Strooper, B.; van Leuven, F.; van den Berghe, H.
 Biochim. Biophys. Acta 1129, 141-143, 1991
 A:Title: The amyloid beta protein precursor or proteinase nexin II from mouse is clos
 A:Reference number: S19727; MUID:92096458; PMID:1756177
 A:Accession: S19727
 A:Molecule type: mRNA
 A:Residues: 1-210, 'G', 212-220, 'S', 222-396, 'A', 398-402, 'T', 404-448, 'A', 450-695 <STR>
 A:Cross-references: EMBL:X59379
 R:izumi, R.; Yamada, T.; Yoshikai, S.; Sasaki, H.; Hattori, M.; Sakaki, Y.
 Gene 112, 189-195, 1992
 A:Title: Positive and negative regulatory elements for the expression of the Alzheim
 A:Reference number: I49485; MUID:92209998; PMID:1555768
 A:Accession: I49485
 A>Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-19 <RES>

A:Cross-references: GB:D10603; NID:g220328; PIDN:BAA01456.1; PID:g220329
 C:Genetics:
 A:Map position: 16C3
 C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase
 C:Keywords: alternative splicing; amyloid; transmembrane protein

Query Match 68.4%; Score 39; DB 2; Length 695;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
 |||||
 DB 620 VGSNKGAI 627

RESULT 12

S00550
 Alzheimer's disease amyloid beta protein precursor - rat
 N:Alternate names: beta-A4 amyloid protein
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 13-Aug-1999
 C:Accession: S00550; A14245; A39820; S46251
 R:Shivers, B.D.; Hilbich, C.; Multhaup, G.; Salbaum, M.; Beyreuther, K.; Seeburg, P.H
 EMBO J. 7, 1365-1370, 1988
 A:Title: Alzheimer's disease amyloidogenic glycoprotein: expression pattern in rat br
 A:Reference number: S00550; MUID:88312583; PMID:2900758
 A:Accession: S00550

A:Molecule type: mRNA
A:Residues: 1-695 <SHI>
A:Cross-references: EMBL:X07648; NID:g555616; PIDN:CAA30488.1; PID:g555617
R:Schubert, D.; Schroeder, R.; LaCordiere, M.; Salton, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430; PMID:2968652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', '39-40', 'X', '42-44' <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor; alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/domain: transmembrane #status predicted <TM>
Query Match 68.4%; Score 39; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VGSNKGAI 9
|||||||
Db 620 VGSNKGAI 627
RESULT 13
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
A:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
A:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AB24853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 68.4%; Score 39; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VGSNKGAI 9
|||||||
Db 672 VGSNKGAI 679
RESULT 14
QRH04
Alzheimer's disease amyloid beta protein precursor [validated] - human
A:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xa inhibitor
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular

protein precursor splice form APP(770)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 28-Jul-1995 #text_change 15-Sep-2000
A:Cross-references: EMBL:X07648; NID:g555616; PIDN:CAA30488.1; PID:g555617
R:Schubert, D.; Schroeder, R.; LaCordiere, M.; Salton, T.; Cole, G.
Science 241, 223-226, 1988
A:Title: Amyloid beta protein precursor is possibly a heparan sulfate proteoglycan core
A:Reference number: A41245; MUID:88264430; PMID:2968652
A:Accession: A41245
A:Molecule type: protein
A:Residues: 18-37, 'X', '39-40', 'X', '42-44' <SCH>
A:Note: evidence for heparan sulfate attachment
R:Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A:Title: The beta-A4 amyloid precursor protein binding to copper.
A:Reference number: S46251; MUID:94320627; PMID:7913895
A:Contents: annotation; copper binding sites
A:Note: rat peptides were isolated but not sequenced
R:Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A:Title: Purification and tissue level of the beta-amyloid peptide precursor of rat brain
A:Reference number: A39820; MUID:91217087; PMID:1673681
A:Accession: A39820
A:Status: preliminary
A:Molecule type: protein
A:Residues: 18-32 <POT>
A:Experimental source: brain
C:Comment: Deposition of amyloid protein as neurofibrillary tangles and/or plaques is characteristic of Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor; alternative splicing; amyloid; glycoprotein; transmembrane protein
F:625-648/domain: transmembrane #status predicted <TM>
Query Match 68.4%; Score 39; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VGSNKGAI 9
|||||||
Db 620 VGSNKGAI 627
RESULT 13
JH0773
Alzheimer's disease amyloid beta protein precursor - African clawed frog
A:Species: Xenopus laevis (African clawed frog)
C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 13-Aug-1999
A:Accession: JH0773
R:Okado, H.; Okamoto, H.
Biochem. Biophys. Res. Commun. 189, 1561-1568, 1992
A:Title: A Xenopus homologue of the human beta-amyloid precursor protein: developmental
A:Reference number: JH0773; MUID:93129227; PMID:1282805
A:Accession: JH0773
A:Molecule type: mRNA
A:Residues: 1-747 <OKA>
A:Cross-references: GB:S52417; NID:g263150; PIDN:AB24853.1; PID:g263151
A:Experimental source: larva
C:Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type proteinase inhibitor
C:Keywords: alternative splicing; amyloid
F:287-337/Domain: animal Kunitz-type proteinase inhibitor homology <BPI>
Query Match 68.4%; Score 39; DB 2; Length 747;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VGSNKGAI 9
|||||||
Db 672 VGSNKGAI 679
RESULT 14
QRH04
Alzheimer's disease amyloid beta protein precursor [validated] - human
A:Alternate names: Alzheimer's disease amyloid A4 protein; coagulation factor Xa inhibitor
N:Contains: amyloid beta protein long, plaque form; amyloid beta protein short, vascular

A:Cross-references: GB:M37896; NID:g178618; PIDN:AAA51727.1; PID:g178620
A:Note: a mutation with 693-Gln is presented
R:Murreli, J.; Farlow, M.; Ghatti, B.; Benson, M.D.
Science 254, 97-99, 1991
A:Title: A mutation in the amyloid precursor protein associated with hereditary Alzheimer
A:Reference number: I59562; MUID:92022553; PMID:1925564
A:Accession: I59562
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 689-716, 'F', 718-737 <MUR>
A:Cross-references: GB:S57665; NID:g236720; PIDN:AAB19991.1; PID:g236721
R:Kamino, K.; Ort, H.T.; Pavani, H.; Wijsman, E.M.; Alonso, M.F.; Pulst, S.M.; Anderson,
araki, S.E.; Korenberg, J.R.; Sharma, V.; Kukull, W.; Larson, E.; Heston, L.L.; Martin,
Am. J. Hum. Genet. 51, 998-1014, 1992
A:Title: Linkage and mutational analysis of familial Alzheimer disease kindreds for the
A:Reference number: A44017; MUID:93035397; PMID:1415269
A:Accession: A44017
A:Molecule type: DNA
A:Residues: 687-692, 'G', 694-718 <KAM1>
A:Cross-references: GB:S45135; NID:g257377; PIDN:AAB3645.1; PID:g257378
A:Experimental source: familial Alzheimer disease family SB
A:Note: sequence extracted from NCBI backbone (NCBIP:115374)
A:Accession: B44017
A:Molecule type: DNA
A:Residues: 687-718 <KAM2>
A:Cross-references: GB:S45136; NID:g257379; PIDN:AAB3646.1; PID:g257380
A:Experimental source: familial Alzheimer disease family LIT
A:Note: sequence extracted from NCBI backbone (NCBIP:115376)
A:Note: this sequence has a silent mutation
R:Kang, J.; Lemaire, H.G.; Unterbeck, A.; Salbaum, J.M.; Masters, C.L.; Grzeschik, K.H.;
Nature 325, 733-736, 1987
A:Title: The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface
A:Reference number: A03134; MUID:87144572; PMID:2881207
A:Accession: A03134
A:Molecule type: mRNA
A:Residues: 1-288, 'V', 365-770 <KAN>
A:Cross-references: GB:Y00264; NID:g28525; PIDN:CAA68374.1; PID:g28526
A:Note: alternative splice form APP(695)
R:Robakis, N.K.; Ramakrishna, N.; Wolfe, G.; Wisniewski, H.M.
Proc. Natl. Acad. Sci. U.S.A. 84, 4190-4194, 1987
A:Title: Molecular cloning and characterization of a cDNA encoding the cerebrovascular A
A:Reference number: A29030; MUID:87231971; PMID:3035574
A:Accession: A29030
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-646, 'E', 648-770 <ROB>
A:Cross-references: GB:M16765; NID:g178539; PIDN:AAA51722.1; PID:g178540
A:Note: the authors translated the codon GAG for residue 647 as Asp
R:Goldgaber, D.; Lerman, M.I.; McBride, O.W.; Saffiotti, U.; Gajdusek, D.C.
Science 235, 877-880, 1987
A:Title: Characterization and chromosomal localization of a cDNA encoding brain amyloid
A:Reference number: A47584; MUID:87120328; PMID:3810169
A:Accession: A47584
A:Molecule type: mRNA
A:Residues: 674-756, 'S', 758-770 <GOL>
A:Cross-references: GB:M15533; NID:g178706; PIDN:AAA35540.1; PID:g178707
A:Experimental source: brain
R:Tanzil, R.E.; Gusella, J.F.; Watkins, P.C.; Bruns, G.A.P.; St George-Hyslop, P.; Van Ke
Science 235, 880-884, 1987
A:Title: Amyloid beta protein gene: cDNA, mRNA distribution, and genetic linkage near th
A:Reference number: A47585; MUID:87120329; PMID:2949367
A:Accession: A47585
A:Molecule type: mRNA
A:Residues: 674-703 <TANI>
A:Cross-references: GB:M15532; NID:g177957; PIDN:AAA51564.1; PID:g177958
R:Dyrks, T.; Weidemann, A.; Multhaup, G.; Salbaum, J.M.; Lemaire, H.G.; Kang, J.; Muelle
EMBO J. 7, 949-957, 1988
A:Title: Identification, transmembrane orientation and biogenesis of the amyloid A4 pred
A:Reference number: S02638; MUID:88226437; PMID:2900137
A:Accession: S02638
A:Molecule type: mRNA
A:Residues: 672-678 <DYR>
R:Tanzil, R.E.; McClatchey, A.I.; Lamperti, E.D.; Villa-Komaroff, L.; Gusella, J.F.; Neve
Nature 331, 528-530, 1988

A:Title: Protease inhibitor domain encoded by an amyloid protein precursor mRNA assoc
A:Reference number: S00707; MUID:88122640; PMID:2893290
A:Accession: S00707
A:Molecule type: mRNA
A:Residues: 286-344, 'I', 365-366 <TAN2>
A:Cross-references: EMBL:X06982; NID:g28817; PIDN:CAA30042.1; PID:g929612
A:Experimental source: promyelocytic leukemia cell line HL60
A:Note: alternative splice form APP(751)
R:Ponte, P.; Gonzalez-DeWhitt, P.; Schilling, J.; Miller, J.; Hsu, D.; Greenberg, B.;
Nature 331, 525-527, 1988
A:Title: A new A4 amyloid mRNA contains a domain homologous to serine proteinase inh
A:Reference number: S00925; MUID:88122639; PMID:2893289
A:Accession: S00925
A:Molecule type: mRNA
A:Residues: 1-344, 'I', 365-770 <PO2>
A:Cross-references: GB:X06989; EMBL:Y00297; NID:g28720; PIDN:CAA30050.1; PID:g28721
A:Note: alternative splice form APP(751)
R:Kitaguchi, N.; Takahashi, Y.; Tokushima, Y.; Shiojiri, S.; Ito, H.
Nature 331, 530-532, 1988
A:Title: Novel precursor of Alzheimer's disease amyloid protein shows protease inhibi
A:Reference number: A38949; MUID:88122641; PMID:2893291
A:Accession: A38949
A:Molecule type: mRNA
A:Residues: 287-367 <KIT>
A:Cross-references: GB:X06981; NID:g28816; PIDN:CAA30041.1; PID:g929611
A:Experimental source: glioblastoma cell line
A:Note: alternative splice form APP(770)
R:Vitek, M.P.; Rasool, C.G.; de Sauvage, F.; Vitek, S.M.; Bartus, R.T.; Beer, B.; Ash
Brain Res. Mol. Brain Res. 4, 121-131, 1988
A:Title: Absence of mutation in the beta-amyloid cDNAs cloned from the brains of thre
A:Reference number: A30320
A:Accession: A30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 284-288, 'V', 365-770 <VIT1>
A:Accession: B30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 122-288, 'V', 365-770 <VIT2>
A:Accession: C30320
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 606-770 <VIT3>
R:Zain, S.B.; Sallm, M.; Chou, W.G.; Sajdel-Sulkowska, E.M.; Majocha, R.E.; Marotta,
Proc. Natl. Acad. Sci. U.S.A. 85, 929-933, 1988
A:Title: Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer disease
A:Reference number: A31087; MUID:88124954; PMID:2893379
A:Accession: A31087
A:Molecule type: mRNA
A:Residues: 507-770 <ZAI>
A:Cross-references: GB:M18734; NID:g178572; PIDN:AAA51726.1; PID:g178573
A:Note: the authors translated the codon GAA for residue 599 as Gly, ACC for residue
8 as Val, GTG for residue 609 as Asn, AAT for residue 610 as Gly, and GGT for residue
A:Note: the cited Genbank accession number, J03594, is not in release 101.0
R:Masters, C.L.; Multhaup, G.; Simms, G.; Potgiesser, J.; Martins, R.N.; Beyreuther,
Query Match 68.4%; Score 39; DB 1; Length 770;
Best Local Similarity 100.0%; Pred.No. 28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 VGSNKGAI 9
|||||
Db 695 VGSNKGAI 702
RESULT 15
T29359
hypothetical protein R0566.9 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29359
R:Murray, J.; Le, T.T.
submitted to the EMBL Data Library, May 1996

A;Description: The sequence of C. elegans cosmid R05G6.
A;Reference number: Z20612
A;Accession: T29359
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-372 <MUR>
A;Cross-references: EMBL:U58746; PIDN:AAB00626.1; GSPDB:GN000022; CESP:R05G6.9
A;Experimental source: strain Bristol N2; clone R05G6
C;Genetics:
A;Gene: CESP:R05G6.9
A;Map position: 4
A;Introns: 80/1; 161/1; 245/1; 286/1

Query Match 66.7%; Score 38; DB 2; Length 372;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CVGSNKGAIC 10
| | | | | : |
Db 139 CVGSKKAPLC 148

Search completed: November 9, 2002, 14:03:42
Job time : 14.8462 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	39	68.4	42	6	US-10-278-181-1	Sequence 1, Appli	
2	39	68.4	595	6	US-10-025-219-1	Sequence 1, Appli	
3	39	68.4	751	6	US-10-025-219-2	Sequence 2, Appli	
4	39	68.4	770	6	US-10-025-219-3	Sequence 3, Appli	
5	35	61.4	260	6	US-10-145-087A-395	Sequence 395, App	
6	35	61.4	260	6	US-10-143-031A-395	Sequence 395, App	
7	35	61.4	260	6	US-10-145-092A-395	Sequence 395, App	
8	35	61.4	260	6	US-10-162-522A-395	Sequence 395, App	
9	35	61.4	260	6	US-10-165-038A-395	Sequence 395, App	
10	35	61.4	260	6	US-10-165-353-395	Sequence 395, App	
11	35	61.4	260	6	US-10-170-481A-395	Sequence 395, App	
12	35	61.4	260	6	US-10-172-039A-395	Sequence 395, App	
13	35	61.4	260	6	US-10-145-016A-395	Sequence 395, App	
14	35	61.4	260	6	US-10-145-088A-395	Sequence 395, App	
15	35	61.4	260	6	US-10-145-139A-395	Sequence 395, App	
16	35	61.4	260	6	US-10-131-813A-396	Sequence 396, App	
17	35	61.4	260	6	US-10-131-819A-396	Sequence 396, App	
18	35	61.4	260	6	US-10-131-823A-396	Sequence 396, App	
19	35	61.4	260	6	US-10-131-824A-396	Sequence 396, App	
20	35	61.4	260	6	US-10-131-826A-396	Sequence 396, App	
21	35	61.4	260	6	US-10-131-829A-396	Sequence 396, App	
22	35	61.4	260	6	US-10-125-926A-396	Sequence 396, App	
23	35	61.4	260	6	US-10-127-829A-396	Sequence 396, App	
24	35	61.4	260	6	US-10-127-831A-396	Sequence 396, App	
25	35	61.4	260	6	US-10-127-835A-396	Sequence 396, App	
26	35	61.4	260	6	US-10-127-837A-396	Sequence 396, App	

6

TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-025-219-3

Query Match 68.4%; Score 39; DB 6; Length 770;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
|||||||
Db 695 VGSNKGAI 702

RESULT 5
US-10-145-087A-395
; Sequence 395, Application US/10145087A
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C47

; CURRENT APPLICATION NUMBER: US/10/145,087A

; CURRENT FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 2001-10-18

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 2001-10-18

; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-087A-395

Query Match 61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGKGA 8
|||||||
Db 198 CAGSSKGA 205

RESULT 6
US-10-143-031A-395
; Sequence 395, Application US/10143031A
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2630P1C39

; CURRENT APPLICATION NUMBER: US/10/143,031A

; CURRENT FILING DATE: 2002-10-10

; PRIOR APPLICATION NUMBER: 09/918585

; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/064249

; PRIOR FILING DATE: 1997-11-03

; PRIOR APPLICATION NUMBER: 60/065311

; PRIOR FILING DATE: 1997-11-13

; PRIOR APPLICATION NUMBER: 60/066364

; PRIOR FILING DATE: 1997-11-21

; PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-03-10

; PRIOR APPLICATION NUMBER: 60/077632

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077641

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11

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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-143-031A-395

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Query Match          61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CVGSNKGK 8
   | |||||
Db 198 CAGSSKGA 205

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RESULT 7
US-10-145-092A-395
; Sequence 395, Application US/10145092A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C45
; CURRENT APPLICATION NUMBER: US/10/145, 092A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-092A-395

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Query Match          61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CVGSNKGK 8
   | |||||
Db 198 CAGSSKGA 205

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RESULT 8
US-10-162-522A-395
; Sequence 395, Application US/10162522A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C56
; CURRENT APPLICATION NUMBER: US/10/162,522A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-162-522A-395

Query Match
Best Local Similarity 61.4%; Score 35; DB 6; Length 260;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGA 8
   | | | | |
Db 198 CAGSSKGA 205

RESULT 9
US-10-165-038A-395
; Sequence 395, Application US/10165038A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C29
; CURRENT APPLICATION NUMBER: US/10/165,038A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-165-038A-395

Query Match
Best Local Similarity 61.4%; Score 35; DB 6; Length 260;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGA 8
   | | | | |
Db 198 CAGSSKGA 205

RESULT 10
US-10-165-353-395
; Sequence 395, Application US/10165353
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C40
; CURRENT APPLICATION NUMBER: US/10/165,353
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649
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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-165-353-395

Query Match 61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGKGA 8
| | | | |
Db 198 CAGSSKGA 205

RESULT 11
US-10-170-481A-395
; Sequence 395, Application US/10170481A
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C53
; CURRENT APPLICATION NUMBER: US/10/170,481A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-481A-395

Query Match 61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGKGA 8
| | | | |
Db 198 CAGSSKGA 205

RESULT 12
US-10-172-039A-395
; Sequence 395, Application US/10172039A
; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C30
; CURRENT APPLICATION NUMBER: US/10/172,039A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

;
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-172-039A-395

Query Match 61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGKGA 8
| 11:111
Db 198 CAGSSKGA 205

RESULT 13

US-10-145-016A-395
; Sequence 395, Application US/10145016A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C52
; CURRENT APPLICATION NUMBER: US/10/145,016A
; CURRENT FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
; PRIOR APPLICATION NUMBER: 60/065311
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: 60/066364
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: 60/077632
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-016A-395

Query Match 61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CVGSNKGKGA 8
| 11:111
Db 198 CAGSSKGA 205

RESULT 14

US-10-145-088A-395
; Sequence 395, Application US/10145088A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C49
; CURRENT APPLICATION NUMBER: US/10/145,088A
; CURRENT FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: 09/918585
; PRIOR FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/064249
; PRIOR FILING DATE: 1997-11-03
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; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: 60/077450
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; PRIOR APPLICATION NUMBER: 60/077641
; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-088A-395

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Query Match      61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CVGSNKGKGA 8
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Db 198 CAGSSKGA 205

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RESULT 15

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US-10-145-129A-395
; Sequence 395, Application US/10145129A
; GENERAL INFORMATION:

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; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

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; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE OF INVENTION: Acids Encoding the Same

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; FILE REFERENCE: P2630PIC51

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; CURRENT APPLICATION NUMBER: US/10/145,129A

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; CURRENT FILING DATE: 2002-10-10

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; PRIOR APPLICATION NUMBER: 09/918585

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; PRIOR FILING DATE: 2001-07-30

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; PRIOR APPLICATION NUMBER: 60/062250

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; PRIOR FILING DATE: 1997-10-17

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; PRIOR APPLICATION NUMBER: 60/064249

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; PRIOR FILING DATE: 1997-11-03

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; PRIOR APPLICATION NUMBER: 60/065311

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; PRIOR FILING DATE: 1997-11-13

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; PRIOR APPLICATION NUMBER: 60/066364

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; PRIOR FILING DATE: 1997-11-21

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; PRIOR APPLICATION NUMBER: 60/077450

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; PRIOR FILING DATE: 1998-03-10

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; PRIOR APPLICATION NUMBER: 60/077632

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; PRIOR FILING DATE: 1998-03-11

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; PRIOR APPLICATION NUMBER: 60/077641

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; PRIOR FILING DATE: 1998-03-11

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; PRIOR APPLICATION NUMBER: 60/077649

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; PRIOR FILING DATE: 1998-03-11
; PRIOR APPLICATION NUMBER: 60/077791
; PRIOR FILING DATE: 1998-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 624
; SEQ ID NO 395
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-145-129A-395

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Query Match      61.4%; Score 35; DB 6; Length 260;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 1 CVGSNKGKGA 8
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Db 198 CAGSSKGA 205

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Search completed: November 9, 2002, 14:11:32
Job time : 5.23077 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2002, 14:03:09 ; Search time 6.15385 Seconds
(without alignments)
23.430 Million cell updates/sec

Title: US-09-632-748-4

Perfect score: 57

Sequence: 1 CVGSNKGAIK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
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3: /cgn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubaa/US06_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	ID	Description
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2	43	75.4	123	10	US-09-771-161A-171
3	39	68.4	8	10	US-09-866-898-1
4	39	68.4	35	10	US-09-867-847-3
5	39	68.4	45	10	US-09-972-475-16
6	39	68.4	40	10	US-09-867-847-2
7	39	68.4	40	10	US-09-988-842-3
8	39	68.4	42	8	US-08-923-055-2
9	39	68.4	42	9	US-09-899-815-1
10	39	68.4	42	10	US-09-867-847-1
11	39	68.4	42	10	US-09-956-625-26
12	39	68.4	42	10	US-09-731-460-1
13	39	68.4	43	10	US-09-280-966-1
14	39	68.4	43	10	US-09-904-987-1
15	39	68.4	43	10	US-09-808-037-3
16	39	68.4	43	10	US-09-866-712-3
17	39	68.4	43	10	US-09-972-475-1
18	39	68.4	43	10	US-09-972-475-3
19	39	68.4	43	10	US-09-992-800-1

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21 39 68.4 43 10 US-09-996-357-1 Sequence 1, Appli
22 39 68.4 43 10 US-09-992-994-1 Sequence 1, Appli
23 39 68.4 43 10 US-09-984-834-1 Sequence 1, Appli
24 39 68.4 43 12 US-10-041-605-1 Sequence 1, Appli
25 39 68.4 49 10 US-09-864-761-33582 Sequence 33582, A
26 39 68.4 49 10 US-09-864-761-34163 Sequence 34163, A
27 39 68.4 53 12 US-09-797-543-5 Sequence 5, Appli
28 39 68.4 53 12 US-10-016-717-1 Sequence 1, Appli
29 39 68.4 55 10 US-09-823-153-10 Sequence 10, Appli
30 39 68.4 70 10 US-09-153-076-14 Sequence 14, Appli
31 39 68.4 100 10 US-09-794-975-4 Sequence 4, Appli
32 39 68.4 103 10 US-09-972-475-2 Sequence 2, Appli
33 39 68.4 103 10 US-09-895-443-2 Sequence 2, Appli
34 39 68.4 104 10 US-09-823-153-4 Sequence 4, Appli
35 39 68.4 117 10 US-09-794-975-6 Sequence 6, Appli
36 39 68.4 117 10 US-09-823-153-2 Sequence 2, Appli
37 39 68.4 355 10 US-09-794-975-13 Sequence 13, Appli
38 39 68.4 695 10 US-09-794-927-10 Sequence 10, Appli
39 39 68.4 695 10 US-09-794-927-12 Sequence 12, Appli
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41 39 68.4 695 10 US-09-795-847-10 Sequence 10, Appli
42 39 68.4 695 10 US-09-795-847-12 Sequence 12, Appli
43 39 68.4 695 10 US-09-795-847-14 Sequence 14, Appli
44 39 68.4 695 10 US-09-794-743-10 Sequence 10, Appli
45 39 68.4 695 10 US-09-794-743-12 Sequence 12, Appli

ALIGNMENTS

RESULT 1
US-09-866-898-4
; Sequence 4, Application US/09866898
; Patent No. US20020051988A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; TITLE OF INVENTION: ALZHEIMER'S DISEASE
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/866,898
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/163,095
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/625,765
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
US-09-866-898-4

Query Match 100.0%; Score 57; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CVGSNKGAIK 10
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Db 1 CVGSNKGAIK 10

RESULT 2
US-09-771-161A-171
; Sequence 171, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:

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; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: VARIANTS OF PROTEIN KINASES
; FILE REFERENCE: 802620-2005.1
; CURRENT APPLICATION NUMBER: US/09/771,161A
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 09/724,676
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 136776
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 135619
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 171
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-771-161A-171

Query Match 75.4%; Score 43; DB 10; Length 123;
Best Local Similarity 60.0%; Pred. No. 0.46;
Matches 6; Conservative 2; Mismatches 0; Indels 2; Gaps 0;

QY 1 CVGSKNGAIC 10
   | | | | | | |
Db 100 CKGGNRGAVC 109

RESULT 3
US-09-866-898-1
; Sequence 1, Application US/09866898
; Patent No. US20020051988A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/866,898
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/163,095
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/625,765
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-898-1

Query Match 68.4%; Score 39; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.7e-04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
   | | | | |
Db 1 VGSNKGAI 8

RESULT 4
US-09-867-847-3
; Sequence 3, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
;
; APPLICANT: LEVINE, et al.
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 35
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-3

Query Match 68.4%; Score 39; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
   | | | | |
Db 24 VGSNKGAI 31

RESULT 5
US-09-972-475-16
; Sequence 16, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/972,475
; FILING DATE: 04-Oct-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,267
; FILING DATE: <Unknown>
; APPLICATION NUMBER: USSN 08/475,579
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: USSN 08/548,998
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A.
; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: PPI-002CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:

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US-09-972-475-16

Query Match 68.4%; Score 39; DB 10; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.67;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
| | | | |
Db 19 VGSNKGAI 26

RESULT 6

US-09-867-847-2
; Sequence 2, Application US/09867847
; Patent No. US2002009433A1
; GENERAL INFORMATION:
; APPLICANT: Chalfour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; TITLE OF INVENTION: AND AMYLOID RELATED DISEASES
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
; OTHER INFORMATION: or peptidomimetics
US-09-867-847-2

Query Match 68.4%; Score 39; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
| | | | |
Db 24 VGSNKGAI 31

RESULT 7

US-09-988-842-3
; Sequence 3, Application US/09988842
; Patent No. US20020143105A1
; GENERAL INFORMATION:
; APPLICANT: Johansson, Jan
; TITLE OF INVENTION: DISCORDANT HELIX STABILIZATION FOR PREVENTION
; TITLE OF INVENTION: OF AMYLOID FORMATION
; FILE REFERENCE: 12125-002001
; CURRENT APPLICATION NUMBER: US/09/988,842
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: US 60/251,662
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/253,695
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-09-988-842-3

Query Match 68.4%; Score 39; DB 10; Length 40;
Best Local Similarity 100.0%; Pred. No. 0.76;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
| | | | |
Db 24 VGSNKGAI 31

RESULT 8

US-08-923-055-2
; Sequence 2, Application US/08923055
; Patent No. US20010016327A1
; GENERAL INFORMATION:
; APPLICANT: Dana Giulian
; TITLE OF INVENTION: Identification of Agents that Protect
; TITLE OF INVENTION: Against Inflammatory Injury to Neurons
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz
; ADDRESSEE: & No. US20010016327A1rls LLP
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WORDPERFECT for WINDOWS 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/923,055
; FILING DATE: Sept-03-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lori Y. Beardsell
; REGISTRATION NUMBER: 34,293
; REFERENCE/DOCKET NUMBER: BYLR-0038
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 42 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-923-055-2

Query Match 68.4%; Score 39; DB 8; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
| | | | |
Db 24 VGSNKGAI 31

RESULT 9

US-09-899-815-1
; Sequence 1, Application US/09899815
; Patent No. US20020162129A1
; GENERAL INFORMATION:
; APPLICANT: LANNFELT, Lars
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF ALZHEIMER'S DISEASE
; FILE REFERENCE: LANNFELT-1A
; CURRENT APPLICATION NUMBER: US/09/899,815
; CURRENT FILING DATE: 2001-07-09

; PRIOR APPLICATION NUMBER: US 60/217,098
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: EP 00202387.7
; PRIOR FILING DATE: 2000-07-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-899-815-1

Query Match 68.4%; Score 39; DB 9; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

RESULT 10
US-09-867-847-1
; Sequence 1, Application US/09867847
; Patent No. US20020094335A1
; GENERAL INFORMATION:
; APPLICANT: Chalifour, Robert
; APPLICANT: Hebert, Lise
; APPLICANT: Kong, Xianqi
; APPLICANT: Gervais, Francine
; TITLE OF INVENTION: VACCINE FOR THE PREVENTION AND TREATMENT OF ALZHEIMER'S
; FILE REFERENCE: 14445-501 CIP
; CURRENT APPLICATION NUMBER: US/09/867,847
; PRIOR FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: 60/168,594
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: 09/724,842
; PRIOR FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: All D peptides
US-09-867-847-1

Query Match 68.4%; Score 39; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

RESULT 11
US-09-956-625-26
; Sequence 26, Application US/09956625
; Patent No. US20020119926A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Paul
; TITLE OF INVENTION: Inhibitors of IAPP Fibril Formation and Uses Thereof
; FILE REFERENCE: 14445-503
; CURRENT APPLICATION NUMBER: US/09/956,625
; PRIOR FILING DATE: 2001-09-19
; PRIOR APPLICATION NUMBER: 60/233,482
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 26
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-956-625-26

Query Match 68.4%; Score 39; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

RESULT 12
US-09-731-460-1
; Sequence 1, Application US/09731460
; Patent No. US20020137112A1
; GENERAL INFORMATION:
; APPLICANT: Chojkier, Mario
; APPLICANT: Buck, Martina
; TITLE OF INVENTION: Compositions and Methods for Diagnosing Alzheimer's
; FILE REFERENCE: CHOJKIER-04302
; CURRENT APPLICATION NUMBER: US/09/731,460
; CURRENT FILING DATE: 2000-12-07
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-731-460-1

Query Match 68.4%; Score 39; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

RESULT 13
US-09-280-966-1
; Sequence 1, Application US/09280966
; Patent No. US20010020097A1
; GENERAL INFORMATION:
; APPLICANT: JAMES E. AUDIA
; BEVERLY K. FOLMER
; VARGHESE JOHN
; JEFFREY S. NISSEN
; WARREN J. PORTER
; EUGENE D. THORSETT
; JING WU
; TITLE OF INVENTION: N-(ARYL/HEROARYLACETYL) AMINO
; ACID ESTERS, PHARMACEUTICAL COMPOSITIONS
; COMPRISING SAME, AND METHODS FOR INHIBITING
; -AMYLOID PEPTIDE RELEASE AND/OR ITS

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESS: Burns, Doane, Swecker & Mathis, LLP
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/280,966
FILING DATE: 30-Mar-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/976,191
FILING DATE: 21 NOV 1997
APPLICATION NUMBER: 60/077,175
FILING DATE: 22 NOV 1996
ATTORNEY/AGENT INFORMATION:
NAME: Swiss, Gerald F.
REGISTRATION NUMBER: 30,113
REFERENCE/DOCKET NUMBER: 002010-335
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-622-2300
TELEFAX: 650-622-2499
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-280-966-1

Query Match 68.4%; Score 39; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

RESULT 14
US-09-904-987-1
Sequence 1, Application US/09904987
Patent No. US20020037908A1
GENERAL INFORMATION:
APPLICANT: NO. US20020037908Alactyl, Inc.
TITLE OF INVENTION: Methods and Compositions for Controlling Pathological and Prepath
FILE OF INVENTION: Protein Assembly or Aggregation
FILE REFERENCE: 42108/26146
CURRENT APPLICATION NUMBER: US/09/904,987
CURRENT FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1
LENGTH: 43
TYPE: PRT
ORGANISM: homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: NCBI ENTREZ / QRHUA4
DATABASE ENTRY DATE: 2000-09-15
RELEVANT RESIDUES: (672)..(714)
US-09-904-987-1

Query Match 68.4%; Score 39; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

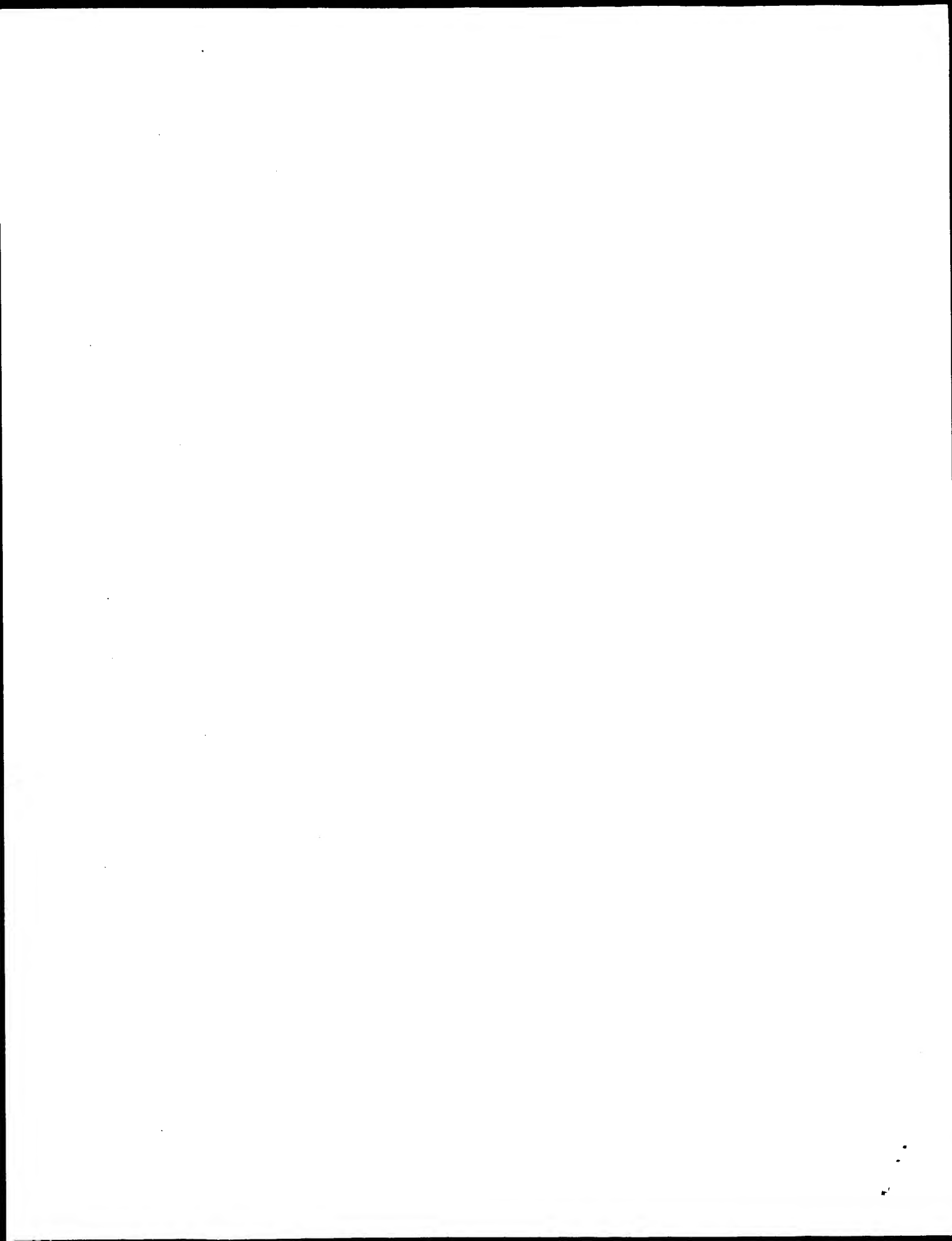
RESULT 15
US-09-808-037-3
Sequence 3, Application US/09808037
Patent No. US20020052311A1
GENERAL INFORMATION:

APPLICANT: SOLOMON, Beka
APPLICANT: HANAN, Eilat
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT AND/OR DIAGNOSIS OF
FILE OF INVENTION: NEUROLOGICAL DISEASES AND DISORDERS
FILE REFERENCE: SOLOMON-2D
CURRENT APPLICATION NUMBER: US/09/808,037
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: 09/629,971
PRIOR FILING DATE: 2000-07-31
PRIOR APPLICATION NUMBER: US 09/473,653
PRIOR FILING DATE: 1999-12-29
PRIOR APPLICATION NUMBER: US 60/152,417
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 43
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-808-037-3

Query Match 68.4%; Score 39; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.82;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VGSNKGAI 9
Db 24 VGSNKGAI 31

Search completed: November 9, 2002, 14:11:55
Job time : 7.15385 secs



GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:04 ; Search time 26.5385 Seconds
(without alignments)
77.641 Million cell updates/sec

Title: US-09-632-748-9

Perfect score: 57

Sequence: 1 CATDIKGAEC 10

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: SP_TREMBL21.*
2: sp_Archea.*
3: sp_Bacteria.*
4: sp_fungi.*
5: sp_human.*
6: sp_invertebrate.*
7: sp_mammal.*
8: sp_mhc.*
9: sp_organelle.*
10: sp_phase.*
11: sp_plant.*
12: sp_rodent.*
13: sp_virus.*
14: sp_vertebrate.*
15: sp_unclassified.*
16: sp_rvirus.*
17: sp_Bacteriap.*
17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	71.9	96	Q9N7I5	Q9n7i5 leishmania
2	39	68.4	145	13 Q9I837	Q9i837 laticauda c
3	38	66.7	385	17 Q8TQ62	Q8tq62 methanosarc
4	38	66.7	1057	4 Q96KR1	Q96kr1 homo sapien
5	38	66.7	2653	5 Q25253	Q25253 lucilia cup
6	36	63.2	189	5 Q8SS05	Q8ss05 encephalito
7	36	63.2	351	11 Q9QZQ5	Q9qzq5 rattus norv
8	36	63.2	512	11 Q9CQ76	Q9cq76 mus muscula
9	35	61.4	145	13 Q9I847	Q9i847 laticauda s
10	35	61.4	145	13 Q9I846	Q9i846 laticauda s
11	35	61.4	145	13 Q9I845	Q9i845 laticauda s
12	35	61.4	145	13 Q9I844	Q9i844 laticauda s
13	35	61.4	145	13 Q9I843	Q9i843 laticauda s
14	35	61.4	145	13 Q9I842	Q9i842 laticauda s
15	35	61.4	145	13 Q9I848	Q9i848 laticauda s
16	35	61.4	154	13 Q8UUh7	Q8uh7 laticauda c

17	35	61.4	155	13 Q8UUI0	Q8uuio laticauda c
18	35	61.4	155	13 Q8UUh9	Q8uuh9 laticauda c
19	35	61.4	194	13 Q9DFE8	Q9dfef8 oncorhynch
20	35	61.4	196	10 Q94H13	Q94h13 oryza sativ
21	35	61.4	271	16 Q92V79	Q92v79 rhizobium m
22	35	61.4	301	10 Q94GB4	Q94gb4 oryza sativ
23	35	61.4	319	5 Q9GV70	Q9gv70 tegula pfei
24	35	61.4	365	12 Q9IR15	Q9ir15 avian ortho
25	35	61.4	365	12 Q9IR14	Q9ir14 avian ortho
26	35	61.4	367	12 Q72463	Q72463 avian ortho
27	35	61.4	367	12 Q9IKC3	Q9ikc3 avian ortho
28	35	61.4	367	12 Q9IKC2	Q9ikc2 avian ortho
29	35	61.4	367	12 Q9IKC1	Q9ikc1 avian ortho
30	35	61.4	367	12 Q9IKC0	Q9ikc0 avian ortho
31	35	61.4	367	12 Q9DLT2	Q9dlt2 avian ortho
32	35	61.4	367	12 Q9DLT0	Q9dlt0 avian ortho
33	35	61.4	367	12 Q9DLT9	Q9dls9 avian ortho
34	35	61.4	367	12 Q9DKH6	Q9dkh6 avian ortho
35	35	61.4	367	12 Q65031	Q65031 avian ortho
36	35	61.4	367	12 Q12284	Q12284 avian reovi
37	35	61.4	430	5 Q76371	Q76371 caenorhabdi
38	35	61.4	442	11 Q99JN8	Q99jn8 mus muscula
39	35	61.4	766	5 Q9V8L3	Q9v8l3 drosophila
40	35	61.4	939	5 Q17685	Q17685 caenorhabdi
41	35	61.4	965	5 Q62275	Q62275 caenorhabdi
42	35	61.4	975	5 Q9N585	Q9n585 caenorhabdi
43	35	61.4	1048	10 Q04938	Q04938 oryza sativ
44	35	61.4	1405	5 Q9N694	Q9n694 toxoplasma
45	34.5	60.5	1383	5 Q19127	Q19127 caenorhabdi

ALIGNMENTS

RESULT 1

Q9N7I5 PRELIMINARY; PRT; 96 AA.
ID Q9N7I5
AC Q9N7I5
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Probable prosbeta3 protein (fragment).
GN LM28.233.
OS Leishmania major.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5664;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FRIDLIN;
RA Murphy L., Quail M., Harris D., Rajandream M., Ivens A., Barrell B.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL390935; CAC00952.1;
DR HSSP; P25451; IRYP.
DR InterPro; IPR001353; Protsme_protease.
DR Fram; PF00227; proteasome; 1.
FT NON_TER 1
FT NON_TER 96
SQ SEQUENCE 96 AA; 10774 MW; E9E76B074C9AE991 CRC64;

Query Match 71.9%; Score 41; DB 5; Length 96;
Best Local Similarity 70.0%; Pred. No. 1.1;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CATDIKGAEC 10
|||: ||:
Db 81 CATDLIGAPC 90

RESULT 2

Q9I837 PRELIMINARY; PRT; 145 AA.
ID Q9I837
AC Q9I837
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 GN Phospholipase A2 precursor (EC 3.1.1.4).
 OS PLA2.
 OS Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea snake).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Laticaudinae; Laticauda.
 OC NCBI_TaxID=8631;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=VENOM GLAND;
 RA Tamiya T., Fujimi T.J.;
 RT "Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cpm09";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Tamiya T., Fujimi T.J.;
 RT "Laticauda semifasciata phospholipase A2 gene clone LsPLA2GL2-1 2-4th exon";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Fujimi T.J., Tsuchiya T., Tamiya T.;
 RT "Comparative analysis of invaded sequences from group I phospholipase A2 genes revealed some evidences about the divergence of the gene groups and families";
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB037415; BAB03302.1; -;
 DR EMBL; AB037219; BAA99510.1; -;
 DR EMBL; AB037218; BAA99510.1; JOINED.
 DR EMBL; AB062439; BAB72246.1; -;
 DR HSP; P00608; 1AE7.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR Pfam: PF00068; Phoslip; 1.
 DR PRINTS; PR00389; PHPLIPASEA2.
 DR ProDom; PD000303; PhospholipaseA2; 1.
 DR SMART; SM00085; PA2C; 1.
 DR PROSITE; PS00119; PA2 ASP; 1.
 DR PROSITE; PS00118; PA2_HTS; 1.
 KW Signal; Hydrolase.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 145 POTENTIAL.
 SQ SEQUENCE 145 AA; 16099 MW; A6245F7CD0ED38F CRC64;

 Query Match 68.4%; Score 39; DB 13; Length 145;
 Best Local Similarity 60.0%; Pred. No. 4.1;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 QY 1 CATDIKGAEC 10
 Db 116 CACDLRAKC 125

 RESULT 3
 ID Q8TQ62 PRELIMINARY; PRT; 385 AA.
 AC Q8TQ62;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Predicted protein.
 GN MAL690.
 OS Methanosarcina acetivorans.
 OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
 OC Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2214;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C2A / ATCC 35395 / DSM 2834;
 RX MEDLINE=21929760; PubMed=11932238;
 RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,

RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A., Allen N., Naylor J., Stange-Thomann N., Dearellano K., Johnson R., Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W., Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M., Hedderich R., Ingram-Smith C., Kuettnner H.C., Krzycki J.A., Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K., Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C., Ferry J.G., Jarrell K.F., Jing H., Macario A.J.D., Paulsen I., Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E., Metcalf W.W., Birren B.;
 RT "The genome of Methanosarcina acetivorans reveals extensive metabolic and physiological diversity";
 RL Genome Res. 12:532-542(2002).
 DR EMBL; AF010842; AAM05097.1; -;
 KW Complete proteome.
 SQ SEQUENCE 385 AA; 43984 MW; 06C276326CECF391 CRC64;

 Query Match 66.7%; Score 38; DB 17; Length 385;
 Best Local Similarity 77.8%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 CATDIKGAEC 9
 Db 17 CLTDDISGAE 25

 RESULT 4
 ID Q96KRL PRELIMINARY; PRT; 1057 AA.
 AC Q96KRL;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Putative zinc finger protein.
 GN ZFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21458566; PubMed=11574164;
 RA Kleines M., Gaertner A., Ritter K., Schaade L.;
 RT "Cloning and expression of the human single copy homologue of the mouse zinc finger protein zfr";
 RL Gene 275:157-162(2001).
 DR EMBL; AJ314790; CAC40818.1; -;
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam; PF00036; zf-C2H2; 3.
 DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; UNKNOWN_3.
 KW DNA-binding; Zinc-finger.
 SQ SEQUENCE 1057 AA; 115287 MW; F7F6C77814146691 CRC64;

 Query Match 66.7%; Score 38; DB 4; Length 1057;
 Best Local Similarity 77.8%; Pred. No. 46;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 2 ATDIKGAEC 10
 Db 495 AEDIKGTGC 503

 RESULT 5
 ID Q25253 PRELIMINARY; PRT; 2653 AA.
 AC Q25253;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Notch homolog scalloped wings (SCL).
 GN SCL.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC	Oscroidae; Calliphoridae; Lucilia.
OX	NCBI_TaxID=7375;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=SS SEEKING;
RX	MEDLINE=96400928; PubMed=8807304;
RA	Davies A.G., Game A.Y., Chen Z., Williams T.J., Goodall S., Yen J.L.,
RA	McKenzie J.A., Batterham P.;
RT	"Scalloped wings is the Lucilia cuprina Notch homologue and a
RT	candidate for the modifier of fitness and asymmetry of diazino
RT	resistance.";
RL	Genetics 143:1321-1337(1996).
RN	[2]
RP	SEQUENCE OF 39-265 FROM N.A.
RC	STRAIN=SS SEEKING;
RA	Chen Z., Newsome T., McKenzie J.A., Batterham P.;
RL	Submitted (DEC-1997) to the EMBL/GenBank/DBDJ databases.
[3]	
RP	SEQUENCE OF 39-265 FROM N.A.
RC	STRAIN=SS SEEKING;
RA	Chen Z., McKenzie J.A., Batterham P.;
EL	Submitted (NOV-1997) to the EMBL/GenBank/DBDJ databases.
DR	EMBL; U58977; AAC36151.1; -.
DR	EMBL; AF032672; AAC36152.1; -.
DR	EMBL; AF032670; AAC36152.1; JOINED.
DR	EMBL; AF032671; AAC36152.1; JOINED.
DR	EMBL; AF032673; AAC36153.1; -.
DR	HSP; P00740; 1EDM.
DR	InterPro; IPR002110; ANK.
DR	InterPro; IPR000152; Asx_hydroxyl.
DR	InterPro; IPR000561; EGF-like.
DR	InterPro; IPR000742; EGF_2.
DR	InterPro; IPR001881; EGF_Ca.
DR	InterPro; IPR001438; EGF_II.
DR	InterPro; IPR000800; Notch.
DR	Pfam; PF00023; ank; 6.
DR	Pfam; PF00008; EGF; 36.
DR	Pfam; PF00066; notch; 3.
DR	PRINTS; PR00010; EGFBL00D.
DR	PRINTS; PR01452; NOTCH.
DR	SMART; SM00248; ANK; 4.
DR	SMART; SM001179; EGF_Ca; 24.
DR	SMART; SM00001; EGF_like; 11.
DR	SMART; SM00004; NL; 2.
DR	PROSITE; PS50088; ANK_REPEAT; 5.
DR	PROSITE; PS50297; ANK_REPEAT_REGION; 1.
DR	PROSITE; PS00010; ASX_HYDROXYL; 22.
DR	PROSITE; PS00022; EGF_1; UNKNOWN_34.
DR	PROSITE; PS01186; EGF_2; 28.
DR	PROSITE; PS01187; EGF_CA; 21.
KW	ANK repeat; Calcium-binding; EGF-like domain; Glycoprotein;
KW	Hydroxylation; Repeat.
SW	SEQUENCE 2653 AA; 285928 MW; 6AF2A058FEEC6329 CRC64;
QY	Query Match 66.7%; Score 38; DB 5; Length 2653;
Db	Best Local Similarity 60.0%; Pred. No. 1.1e-02;
	Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps
QY	1 CATDIKGAEC 10
Db	418 CATGYKGVDC 427
RESULT 6	
Q8SS05	
ID	Q8SS05 PRELIMINARY; PRT; 189 AA.
AC	Q8SS05;
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	40S ribosomal protein S3A (lysine-rich KRP-A) (S1 in yeast).
GN	ECU05_0250.

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Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATDIKGAEC 10
    |||:|:|
Db 250 ATDMKGRKC 258

RESULT 8
Q9C076 PRELIMINARY; PRT; 512 AA.
AC Q9C076;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE 5730521E12Rik protein.
GN 5730521E12RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=EMBRYO;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Felschmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher M., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kaniya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AK017780; BAB30928.1; -.
DR EMBL: AK017656; BAB30857.1; -.
DR MGD: MGI:1913900; 5730521E12Rik.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR000483; LRR_Cterm.
DR InterPro: IPR000372; LRR_Nterm.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR003591; LRR_typ.
DR Pfam: PF00560; LRR; 10.
DR Pfam: PF01463; LRRCT; 1.
DR PRINTS: PR00019; LEURICRPT.
DR SMART: SM00370; LRR; 4.
DR SMART: SM00082; LRRCT; 1.
DR SMART: SM00013; LRRNT; 1.
DR SMART: SM00369; LRR_TYP; 9.
SQ SEQUENCE 512 AA; 57704 MW; BA8F0C4B6F809FAF CRC64;

Query Match 63.2%; Score 36; DB 11; Length 512;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 TDIKGAEC 10
    ||:|:|
Db 445 TDVKGQC 452

RESULT 9
Q9I847 PRELIMINARY; PRT; 145 AA.
AC Q9I847;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Phospholipase A2 precursor.
GN PLA2.
OS Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
OS snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Tamiya T., Fujimi T.J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RE EMBL: AB037409; BAB03296.1; -.
DR HSSP: P00608; IAE7.
DR InterPro: IPR001211; PhospholipaseA2.
DR Pfam: PF00068; phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PRODOM: PD000303; PhospholipaseA2; 1.
DR SMART: SM00085; PA2c; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
DR PROSITE: PS00118; PA2_HIS; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 145 AA; 16062 MW; D3BC01790A0F7885 CRC64;

Query Match 61.4%; Score 35; DB 13; Length 145;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CADIKGAEC 10
    ||:|:|
Db 116 CACDLQAAC 125

RESULT 10
Q9I846 PRELIMINARY; PRT; 145 AA.
AC Q9I846;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Phospholipase A2 precursor.
GN PLA2.
OS Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
OS snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Tamiya T., Fujimi T.J.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RE EMBL: AB037410; BAB03297.1; -.
DR HSSP: P00608; IAE7.
DR InterPro: IPR001211; PhospholipaseA2.
DR Pfam: PF00068; phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PRODOM: PD000303; PhospholipaseA2; 1.
DR SMART: SM00085; PA2c; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
DR PROSITE: PS00118; PA2_HIS; 1.
KW Signal.
FT SIGNAL.
SQ SEQUENCE 145 AA; 16062 MW; D3BC01790A0F7885 CRC64;

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SQ SEQUENCE 145 AA; 16059 MW; 9277AC82B50F7887 CRC64;
 Query Match 61.4%; Score 35; DB 13; Length 145;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY      1 CATDIKGAEC 10
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Db       116 CACDLOAAKC 125

RESULT 11
Q9I845
ID      Q9I845 PRELIMINARY; PRT; 145 AA.
AC      Q9I845;
DT      01-OCT-2000 (TtEMBLrel. 15, Created)
DT      01-OCT-2000 (TtEMBLrel. 15, Last sequence update)
DT      01-JUN-2002 (TtEMBLrel. 21, Last annotation update)
DE      Phospholipase A2 precursor.
DE      PLA2.
GN      Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
OS      snake).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC      Elapidae; Laticaudinae; Laticauda.
NCBI_TaxID=8631;
RN      [1]
RX      SEQUENCE FROM N.A.
RP      TISSUE=VENOM GLAND.
RC      Tamiya T., Fujimi T.J.;
RA      "Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cPt09.";
RL      Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AB037411; BAB03298.1; -
DR      HSSP; P00608; IAE7.
DR      InterPro; IPR001211; PhospholipaseA2.
DR      Pfam; PF00068; phoslip; 1.
DR      PRINTS; PR00389; PHPLIPASEA2.
DR      ProDom; PD000303; PhospholipaseA2; 1.
DR      SMART; SM00085; PA2c; 1.
DR      PROSITE; PS00119; PA2_ASP; 1.
DR      DR PROSITE; PS00118; PA2_HIS; 1.
KW      Signal.
FT      SIGNAL.
SQ      SEQUENCE 1 27 POTENTIAL.

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Query Match 61.4%; Score 35; DB 13; Length 145;
 Best Local Similarity 50.0%; Pred. No. 27;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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QY      1 CATDIKGAEC 10
|||::|:|
Db       116 CACDLOAAKC 125

RESULT 12
Q9I844
ID      Q9I844 PRELIMINARY; PRT; 145 AA.
AC      Q9I844;
DT      01-OCT-2000 (TtEMBLrel. 15, Created)
DT      01-OCT-2000 (TtEMBLrel. 15, Last sequence update)
DT      01-JUN-2002 (TtEMBLrel. 21, Last annotation update)
DE      Phospholipase A2 precursor.
DE      PLA2.
GN      Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
OS      snake).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC      Elapidae; Laticaudinae; Laticauda.
NCBI_TaxID=8631;
RN      [1]
RX      SEQUENCE FROM N.A.
RP      TISSUE=VENOM GLAND;
RC      Tamiya T., Fujimi T.J.;
RA

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DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase A2 precursor.
GN PLA2.
OS Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8631;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=VENOM GLAND;
RA Tamiya T., Fujimi T.J.;
RT "Laticauda semifasciata phospholipase A2 cDNA clone LsPLA2cPm08.";
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB037414; BAB03301.1; -.
DR HSSP; P00608; 1AE7.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Signal.
FT SIGNAL
FT SIGNAL
SQ SEQUENCE 145 AA; 16085 MW; 6626FDC7AE0ED39D CRC64;

Query Match 61.4%; Score 35; DB 13; Length 145;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
|||::|:|
Db 116 CACDLQAAC 125

Search completed: November 9, 2002, 14:03:02
Job time : 28.5385 secs

RESULT 15
QI848
ID Q91848 PRELIMINARY; PRT; 145 AA.
AC Q91848;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phospholipase A2 precursor (EC 3.1.1.4).
GN PLA2
OS Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8631;
RN [1]
RP SEQUENCE FROM N.A.
RA Fujimi T.J., Tsuchiya T., Tamiya T.;
RT "Comparative analysis of invaded sequences from group I phospholipase
RT A2 genes revealed some evidences about the divergence of the gene
RT groups and families."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062440; BAB72247.1; -.
DR HSSP; P00608; 1AE7.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Signal; Hydrolase.
FT SIGNAL
FT SIGNAL
SQ SEQUENCE 145 AA; 15900 MW; 1F84DF6F7BC5348F CRC64;

Query Match 61.4%; Score 35; DB 13; Length 145;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
|||::|:|
Db 116 CACDLQAAC 125

Search completed: November 9, 2002, 14:03:02
Job time : 28.5385 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:57:44 ; Search time 7.69231 Seconds
(without alignments)
53.919 Million cell updates/sec

Title: US-09-632-748-9

Perfect score: 57

Sequence: 1 CATDIKGAEC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	DB ID	Description
1	41	71.9	205	1 PSB3_TRYBB	Q9ndal trypanosoma
2	38	66.7	362	1 MOM2_CABEL	Q10459 caenorhabdi
3	38	66.7	963	1 UBP4_HUMAN	Q13107 homo sapien
4	38	66.7	1035	1 TAC2_MOUSE	Q9jj90 mus musculu
5	38	66.7	2703	1 NOTC_DRONE	P07207 drosophila
6	35	61.4	118	1 PA21_LATSE	P00611 laticauda s
7	35	61.4	118	1 PA23_LATSE	P00612 laticauda s
8	35	61.4	119	1 PA24_LATSE	P00613 laticauda s
9	35	61.4	119	1 PA21_OXYSC	P00614 oxyuranus s
10	35	61.4	404	1 PRSB_XENLA	O42586 xenopus lae
11	35	61.4	439	1 PRSA_HUMAN	P17980 homo sapien
12	35	61.4	439	1 PRSA_RAT	Q63569 rattus norv
13	35	61.4	1124	1 TIE2_HUMAN	Q02763 homo sapien
14	35	61.4	1125	1 TIE2_BOVIN	Q06807 bos taurus
15	34	59.6	229	1 NGF_PIG	Q29074 sus scrofa
16	34	59.6	231	1 NGF_BOVIN	P13600 bos taurus
17	34	59.6	231	1 NGF_XENLA	P21617 xenopus lae
18	34	59.6	241	1 NGF_CAVPO	P19093 cavia porce
19	34	59.6	241	1 NGF_HUMAN	P01138 homo sapien
20	34	59.6	241	1 NGF_MOUSE	P01139 mus musculu
21	34	59.6	241	1 NGF_RAT	P25427 rattus norv
22	34	59.6	243	1 NGF_CHICK	P05200 gallus gall
23	34	59.6	254	1 PSA7_YEAST	P40303 saccharomyc
24	34	59.6	322	1 ASPG_BACLI	P30363 bacillus li
25	34	59.6	341	1 RTCA_PSEAE	Q9hv19 pseudomonas
26	34	59.6	373	1 CK13_HUMAN	O02833 homo sapien
27	34	59.6	379	1 P2X6_MOUSE	O54803 mus musculu
28	34	59.6	379	1 P2X6_RAT	P51579 rattus norv
29	34	59.6	534	1 UD13_HUMAN	P35503 homo sapien
30	34	59.6	534	1 UD14_HUMAN	P22310 homo sapien
31	34	59.6	534	1 UD15_HUMAN	P35504 homo sapien
32	33	57.9	81	1 YU61_HALN1	O54608 halobacteri
33	33	57.9	106	1 CY2_RHOGL	P00080 rhodospila 9

ALIGNMENTS

RESULT 1

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PSB3_TRYBB
ID PSB3_TRYBB STANDARD; PRT; 205 AA.
AC Q9NDAL;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proteasome subunit beta type 3 (EC 3.4.25.1) (20S proteasome subunit
DE beta-3).
DE PSB3.
GN Trypanosoma brucei brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5702;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=427;
RA Bozdech Z., Huang L., Yao Y., Morton A., Wang C.C.;
RT "TbPSB3-beta 3 subunit of 20S proteasome from T. brucei.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH ARG,
CC PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT NEUTRAL OR
CC SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT PROTEOLYTIC
CC ACTIVITY (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Cleavage at peptide bonds with very broad
CC specificity.
CC -1- PATHWAY: Involved in an ATP/ubiquitin-dependent non-lysosomal
CC proteolytic pathway.
CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (By similarity).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B.
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EMBL; AF169653; AAF89685.1; -
HSSP; P25451; IRYP.
InterPro; IPR000243; Proteasome_B.
InterPro; IPR001353; Proteasome.
DR Pfam; PF00227; proteasome; 1.
DR PROSITE; PS00854; PROTEASOME_B; FALSE_NEG.
KW Proteasome; Hydrolase; Protease.
SQ SEQUENCE 205 AA; 22458 MW; 4CB2093E81E2FFD7 CRC64;

```

Query Match 71.9%; Score 41; DB 1; Length 205;

Best Local Similarity 70.0%; Pred. No. 0.8;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

Db 122 CATDLIGAPC 131
|||||

RESULT 2

MOM2 CAEEL STANDARD; PRT; 362 AA.
AC Q10459; 016146;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE MOM-2 protein precursor.
GN MOM-2 OR F38E1.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE-97433081; PubMed-9288750;
RA Rocheleau C.E., Downs W.D., Lin R., Wittmann C., Bei Y., Cha Y.-H.,
RA Ali M., Pries J.R., Mello C.C.;
RT "Wnt signaling and an APC-related gene specify endoderm in early C.
RT elegans embryos."
RL Cell 90:707-716(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Gattung S., Le T.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP REVISIONS.
RA Waterston R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
CC TRANSMEMBRANE RECEPTORS. PROBABLE DEVELOPMENTAL PROTEIN INVOLVED
CC IN ENDODERM SPECIFICATION AND CLEAVAGE AXIS DETERMINATION.
CC -!- SUBCELLULAR LOCATION: Possibly secreted and associates with the
CC extracellular matrix.
CC -!- SIMILARITY: BELONGS TO THE WNT FAMILY.

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CC -----
DR EMBL; AF013952; AAC47749.1; -;
DR EMBL; U41996; AAA83472.2; -;
DR WormPep; F38E1.7; CE17806.
DR InterPro; IPR000970; Wnt_grthfactor.
DR Pfam; PF00110; Wnt; 1.
DR SMART; SM00097; WNT1; 1.
DR PROSITE; PS00246; WNT1; 1.
DR Developmental protein; Glycoprotein; Signal.
FT SIGNAL 1 24
FT CHAIN 25 362 MOM-2 PROTEIN.
FT CARBOHYD 90 90 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 362 AA; 40190 MW; ED69435F1F4F40DD CRC64;

Query Match 66.7%; Score 38; DB 1; Length 362;
Best Local Similarity 60.0%; Pred. No. 5.1;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CATDLIGAPC 10
||| | | |
DB 304 CAIDVKDREC 313

RESULT 3

UBP4_HUMAN

UBP4_HUMAN STANDARD; PRT; 963 AA.
AC Q13107; O43452; O43453;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase 4 (EC 3.1.2.15) (Ubiquitin
DE thiolesterase 4) (Ubiquitin-specific processing protease 4)
DE (Deubiquitinating enzyme 4) (Ubiquitous nuclear protein homolog).
GN USP4 OR UNP OR UNPH.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE-95303480; PubMed-7784062;
RA Gray D.A., Inazawa J., Gupta K., Wong A., Ueda R., Takahashi T.;
RT "Elevated expression of Unph, a proto-oncogene at 3p21.3, in human
RT lung tumors."
RL Oncogene 10:2179-2183(1995).
RN [2]
RP REVISIONS.
RA Gray D.A.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-98124180; PubMed-9464533;
RA Frederick A., Rolfe M., Chlu M.I.;
RT "The human UNP locus at 3p21.31 encodes two tissue-selective,
RT cytoplasmic isoforms with deubiquitinating activity, that have reduced
RT expression in small cell lung carcinoma cell lines."
RL Oncogene 16:153-165(1998).
CC -!- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; UNPCL (SHOWN HERE) AND UNPES;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19.
CC -----
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CC -----
DR EMBL; U20657; AAB72237.1; -;
DR EMBL; AF017305; AAC27355.1; -;
DR EMBL; AF017306; AAC27356.1; -;
DR MEROPS; C19.010; -;
DR Genew; HGNC:12627; USP4.
DR MIM; 603486; -;
DR InterPro; IPR001394; UCH-2.
DR Pfam; PF00442; UCH-1; 1.
DR Pfam; PF00443; UCH-2; 1.
DR PROSITE; PS00972; UCH_2_1; 1.
DR PROSITE; PS00973; UCH_2_2; 1.
DR PROSITE; PS0235; UCH_2_3; 1.
KW Ub1 conjugation pathway; Hydrolase; Thiol protease; Multigene family;
KW Proto-oncogene; Alternative splicing.
FT ACT_SITE 311 311
FT ACT_SITE 873 873
FT ACT_SITE 881 881
FT VARSPLIC 232 279
FT FT
FT MUTAGEN 311 311 BY SIMILARITY.
FT MUTAGEN 373 373 BY SIMILARITY.
FT CONFLICT 744 744 KSTAPSRNFTTSPKSSASPYSVSASLIANGDS*STCGMH
FT CONFLICT 963 AA; 108564 MW; 1B62B752F9410CD7 CRC64;
SQ SEQUENCE

Query Match 66.7%; Score 38; DB 1; Length 963;
 Best Local Similarity 50.0%; Pred. No. 12;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
 I: | : | : |
 Db 568 CSTSVGSGEC 577

RESULT 4

TAC2_MOUSE
 ID TAC2_MOUSE STANDARD; PRT; 1035 AA.
 AC Q9JUG0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Transforming acidic coiled-coil-containing protein 2.
 GN TAC2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RA Osada N., Kusuda J., Tanuma R., Ito A., Hirata M., Sugano S.,
 RA Hashimoto K.;
 RT "Isolation of full-length cDNA clones from mouse brain cDNA library
 RT made by oligo-capping method";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: MAY PLAY A ROLE IN ORGANIZING CENTROSOMAL MICROTUBULES.
 CC MAY ACT AS A TUMOR SUPPRESSOR PROTEIN (BY SIMILARITY).
 CC -!- SUBUNIT: INTERACTS WITH MICROTUBULES (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: NUCLEAR; CONCENTRATED AT CENTROSOMES (BY
 CC SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE TACC FAMILY.
 CC
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 CC
 CC EMBL; AB041546; BAA95031.1; -
 DR HSSP; P02649; 1LE4.
 DR MGD; MGI:1928899; Tacc2.
 KW Coiled coil; Nuclear protein.
 FT DOMAIN 43 51 POLY-PRO.
 FT DOMAIN 496 499 POLY-LYS.
 FT DOMAIN 763 791 COILED COIL (POTENTIAL).
 FT DOMAIN 834 1034 COILED COIL (POTENTIAL).
 SQ SEQUENCE 1035 AA; 112715 MW; 0698015282F94C78 CRC64;

Query Match 66.7%; Score 38; DB 1; Length 1035;
 Best Local Similarity 60.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
 I: | : | : |
 Db 134 CSADSKGQEC 143

RESULT 5

NOTC_DROME
 ID NOTC_DROME STANDARD; PRT; 2703 AA.
 AC P07207; P04154; O97458; Q9W478;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Neurogenic locus Notch protein precursor.
 GN N OR EG:140G11.1 OR EG:163A10.2 OR CG3936.

OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R; TISSUE=Embryo;
 RX MEDLINE=86079539; PubMed=3935325;
 RA Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
 RT "Nucleotide sequence from the neurogenic locus notch implies a gene
 RT product that shares homology with proteins containing EGF-like
 RT repeats.";
 RL Cell 43:567-581(1985).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Canton-S, and Oregon-R; TISSUE=Embryo;
 RX MEDLINE=87064624; PubMed=3097517;
 RA Kidd S., Kelley M.R., Young M.W.;
 RT "Sequence of the notch locus of Drosophila melanogaster: relationship
 RT of the encoded protein to mammalian clotting and growth factors.";
 RL Mol. Cell. Biol. 6:3094-3108(1986).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostel A., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Oregon-R;
 RX MEDLINE=20196011; PubMed=10731137;
 RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
 RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
 RA Dreano S., Gloux S., Lelaure V., Mottier S., Mottier S., Borkova D.,
 RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
 RA Papadogiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,

RA Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RT melanogaster.";
RL Science 287:2220-2222(2000).
RN [5]
RN SEQUENCE OF 1-8 FROM N.A.
RX MEDLINE=8509329; PubMed=2981631;
RA Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S.;
RT "opa: a novel family of transcribed repeats shared by the Notch locus
RT and other developmentally regulated loci in D. melanogaster.";
RL Cell 40:55-62(1985).
RN [6]
RN SEQUENCE OF 1-8 FROM N.A.
RX MEDLINE=87257846; PubMed=3037327;
RA Kelley M.R., Kidd S., Berg R.L., Young M.W.;
RT "Restriction of P-element insertions at the Notch locus of Drosophila
RT melanogaster.";
RL Mol. Cell. Biol. 7:1545-1548(1987).
RN [7]
RN REVIEW.
RA Harris W.A.;
RT "Many cell types specified by Notch function.";
RL Curr. Biol. 1:120-122(1991).
CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands Delta
CC and Serrate to regulate cell-fate determination. Upon ligand
CC activation through the released notch intracellular domain (NICD)
CC it forms a transcriptional activator complex with Su(H)
CC (Suppressor of hairless) and activates genes of the enhancer of
CC split locus. Essential for proper differentiation of ectoderm.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC -!- SIMILARITY: CONTAINS 36 EGF-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
CC -!- SIMILARITY: CONTAINS 6 ANK REPEATS.
CC -----
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DR EMBL; M16152; AAB59220.1; -;
DR EMBL; M16153; AAB59220.1; JOINED.
DR EMBL; M16149; AAB59220.1; JOINED.
DR EMBL; M16150; AAB59220.1; JOINED.
DR EMBL; M16151; AAB59220.1; JOINED.
DR EMBL; M16151; AAB59220.1; JOINED.
DR EMBL; K03508; AAB28725.1; -;
DR EMBL; M13689; AAB28725.1; JOINED.
DR EMBL; K03507; AAB28725.1; JOINED.
DR EMBL; AE003426; AAF45848.2; -;
DR EMBL; AL035436; CAB37610.1; -;
DR EMBL; AL035395; CAB37610.1; JOINED.
DR EMBL; M12175; AAB74496.1; -;
DR EMBL; M16025; AAB28726.1; -;
DR PIR; A24420; A24420.
DR PIR; A24768; A24768.
DR PIR; A05267; A05267.
DR HSP; P00740; IEDM.
DR FlyBase; FBgn0004647; N.
DR InterPro; IPR002110; ANK.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR000742; EGF-2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR000800; Notch.

DR Pfam; PF00008; EGF; 36.
DR Pfam; PF00023; ank; 6.
DR Pfam; PF00066; notch; 3.
DR PRINTS; PR00010; EGF_BLOOD.
DR PRINTS; PR00011; EGF_LAMININ.
DR PRINTS; PR01452; NOTCH.
DR SMART; SM00248; ANK; 7.
DR SMART; SM00181; EGF; 36.
DR SMART; SM00179; EGF_CA; 35.
DR SMART; SM00004; NL; 2.
DR PROSITE; PS00088; ANK_REPEAT; 5.
DR PROSITE; PS0297; ANK_REPEAT_REGION; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 22.
DR PROSITE; PS00022; EGF_1; 34.
DR PROSITE; PS01186; EGF_2; 28.
DR PROSITE; PS01187; EGF_CA; 21.
KW Receptor; transcription regulation; Activator; Differentiation;
KW Developmental protein; Neurogenesis; Repeat; ANK repeat;
KW EGF-like domain; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 44 POTENTIAL.
FT CHAIN 45 2703 NEUROGENIC LOCUS NOTCH PROTEIN.
FT DOMAIN 45 1745 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1746 1766 POTENTIAL.
FT DOMAIN 1767 2703 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 58 95 EGF-LIKE 1.
FT DOMAIN 96 136 EGF-LIKE 2.
FT DOMAIN 139 176 EGF-LIKE 3.
FT DOMAIN 177 215 EGF-LIKE 4.
FT DOMAIN 217 253 EGF-LIKE 5.
FT DOMAIN 255 291 EGF-LIKE 6.
FT DOMAIN 293 329 EGF-LIKE 7.
FT DOMAIN 331 370 EGF-LIKE 8.
FT DOMAIN 372 408 EGF-LIKE 9.
FT DOMAIN 409 447 EGF-LIKE 10.
FT DOMAIN 449 486 EGF-LIKE 11.
FT DOMAIN 488 524 EGF-LIKE 12.
FT DOMAIN 526 562 EGF-LIKE 13.
FT DOMAIN 564 600 EGF-LIKE 14.
FT DOMAIN 602 637 EGF-LIKE 15.
FT DOMAIN 639 675 EGF-LIKE 16.
FT DOMAIN 677 713 EGF-LIKE 17.
FT DOMAIN 715 751 EGF-LIKE 18.
FT DOMAIN 753 789 EGF-LIKE 19.
FT DOMAIN 791 827 EGF-LIKE 20.
FT DOMAIN 829 865 EGF-LIKE 21.
FT DOMAIN 867 905 EGF-LIKE 22.
FT DOMAIN 907 944 EGF-LIKE 23.
Query Match 66.7%; Score 38; DB 1; Length 2703;
Best Local Similarity 60.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 CATDIRGAEC 10
Db 437 CATGYRGVDC 446
RESULT 6
PA21_LATSE STANDARD; PRT; 118 AA.
ID PA21_LATSE
AC P00611;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phospholipase A2 isozyme I (EC 3.1.1.4) (Phosphatidylcholine
DE 2-acylhydrolase).
OS Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
OS snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8631;
RN [1]


```

RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=83153048; PubMed=7165712;
RA Nishida S., Kim H.S., Tamiya N.;
RT "Amino acid sequences of three phospholipases A I, III and IV from
the venom of the sea snake Laticauda semifasciata.";
RL Biochem. J. 207:589-594(1982).
RN [2]
RP REVIEWS TO 70-80.
RX MEDLINE=89044898; PubMed=3188064;
RA Takasaki C., Kuramochi H., Shimazu T., Tamiya N.;
RT "Correction of amino acid sequence of phospholipase A2 I from the
venom of Laticauda semifasciata (Erabu sea snake).";
RL Toxicon 26:747-749(1988).
RN [2]
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
2-ACYL GROUPS IN 3-SN-PHOSPHOLIPASES.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR PIR: A00752; PSLT1E.
DR HSP: P00608; IAE7.
DR InterPro: IPR001211; PhospholipaseA2.
DR Pfam: PF00068; Phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PRODOM: PD000303; PhospholipaseA2; 1.
DR SMART: SM00085; PA2c; 1.
DR PROSITE: PS00118; PA2_HIS; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
DR Hydrolase: Lipid degradation; Calcium; Multigene family; Venom.
FT ACT_SITE 48 64
FT ACT_SITE 64 64
FT ACT_SITE 92 92
FT DISULFID 11 71
FT DISULFID 27 117
FT DISULFID 29 45
FT DISULFID 44 98
FT DISULFID 51 91
FT DISULFID 60 84
FT DISULFID 78 89
FT CA_BIND 28 30
FT CA_BIND 30 30
FT CA_BIND 32 32
FT CA_BIND 49 49
FT SEQUENCE 118 AA; 13131 MW; F3BC43C215B89CD CRC64;
Query Match 61.4%; Score 35; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. NO. 6.9;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 CATDIKGAEC 10
DB 89 CACDLEAAKC 98
|||:::|:|
|||:::|:|

RESULT 7
PA23_LATSE STANDARD; PRT; 118 AA.
AC P00612;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phospholipase A2 isozyme III (EC 3.1.1.4) (Phosphatidylcholine 2-
acylhydrolase).
OS Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8631;
RN [1]

```

```

RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=83153048; PubMed=7165712;
RA Nishida S., Kim H.S., Tamiya N.;
RT "Amino acid sequences of three phospholipases A I, III and IV from
the venom of the sea snake Laticauda semifasciata.";
RL Biochem. J. 207:589-594(1982).
RN [2]
CC -1- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
2-ACYL GROUPS IN 3-SN-PHOSPHOLIPASES.
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
acylglycerophosphocholine + a fatty acid anion.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR PIR: A00753; PSLT3E.
DR HSP: P00608; IAE7.
DR InterPro: IPR001211; PhospholipaseA2.
DR Pfam: PF00068; Phoslip; 1.
DR PRINTS: PR00389; PHPLIPASEA2.
DR PRODOM: PD000303; PhospholipaseA2; 1.
DR SMART: SM00085; PA2c; 1.
DR PROSITE: PS00118; PA2_HIS; 1.
DR PROSITE: PS00119; PA2_ASP; 1.
DR Hydrolase: Lipid degradation; Calcium; Multigene family; Venom.
FT ACT_SITE 48 48
FT ACT_SITE 92 92
FT DISULFID 11 71
FT DISULFID 27 117
FT DISULFID 29 45
FT DISULFID 44 98
FT DISULFID 51 91
FT DISULFID 60 84
FT DISULFID 78 89
FT CA_BIND 28 30
FT CA_BIND 30 30
FT CA_BIND 32 32
FT CA_BIND 49 49
FT SEQUENCE 118 AA; 13243 MW; CCF5671A8851560B CRC64;
Query Match 61.4%; Score 35; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. NO. 6.9;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 CATDIKGAEC 10
DB 89 CACDLEAAKC 98
|||:::|:|
|||:::|:|

RESULT 8
PA24_LATSE STANDARD; PRT; 118 AA.
AC P00613;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phospholipase A2 isozyme IV (EC 3.1.1.4) (Phosphatidylcholine 2-
acylhydrolase).
OS Laticauda semifasciata (Broad-banded blue sea snake) (Erabu sea
snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Laticaudinae; Laticauda.
OX NCBI_TaxID=8631;
RN [1]

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DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_centri.
DR InterPro; IPR003960; AAA_sub.
DR Pfam; PF00004; AAA; 1.
DR SMART; SM00382; AAA; 1.
DR TIGRFAMs; TIGR01242; 26Sp45; 1.
DR PROSITE; PS00674; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
DR NP_BIND; 192 199 ATP (POTENTIAL).
DR SEQUENCE 404 AA; 45276 MW; FC988BBBDCFC2E3 CRC64;

Query Match 61.4%; Score 35; DB 1; Length 404;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
DB 352 CTDDFNGAQC 361

RESULT 11
PRSA_HUMAN STANDARD; PRT; 439 AA.
AC P17980; Q96HD3;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 26S protease regulatory subunit 6A (Tat-binding protein 1) (TBP-1)
DE (Proteasome subunit P50).
GN PSMC3 OR TBPI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93126329; PubMed=8419915;
RA Ohana B., Moore P.A., Ruben S.M., Southgate C.D., Green M.R.,
RA Rosen C.A.;
RT "The type I human immunodeficiency virus Tat binding protein is a
RT transcriptional activator belonging to an additional family of
RT evolutionarily conserved genes."
RL Proc. Natl. Acad. Sci. U.S.A. 90:138-142(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 36-439 FROM N.A.
RX MEDLINE=90302011; PubMed=2194290;
RA Nelbock P., Dillon P.J., Perkins A., Rosen C.A.;
RT "A cDNA for a protein that interacts with the human immunodeficiency
RT virus Tat transactivator."
RL Science 248:1650-1653(1990).
RN [4]
RP PARTIAL SEQUENCE.
RX MEDLINE=96216387; PubMed=8621709;
RA Denartino G.N., Proske R.J., Moomaw C.R., Strong A.A., Song X.,
RA Hisamatsu H., Tanaka K., Slaughter C.A.;
RT "Identification, purification, and characterization of a
RT P4700-dependent activator of the proteasome."
RL J. Biol. Chem. 271:3112-3118(1996).
CC -!- FUNCTION: THE 26S PROTEASE IS INVOLVED IN THE ATP-DEPENDENT
CC DEGRADATION OF UBIQUITINATED PROTEINS. THE REGULATORY (OR ATPASE)
CC COMPLEX CONFERS ATP DEPENDENCY AND SUBSTRATE SPECIFICITY TO THE
CC 26S COMPLEX (BY SIMILARITY).
CC -!- FUNCTION: INTERACTS WITH THE HUMAN IMMUNODEFICIENCY VIRUS TAT
CC TRANSACTIVATOR. SPECIFICALLY SUPPRESSES TAT-MEDIATED
CC TRANSCRIPTION. PROBABLY INVOLVED IN ATP HYDROLYSIS. IT IS
CC POSSIBLE THAT PROTEINS MSI AND TBP-1 COMPETE WITH EACH OTHER TO
CC REGULATE THE INTERACTION WITH THE TRANSCRIPTIONAL COMPLEX WITH THE
CC HIV GENE, THEREBY INFLUENCING GENE EXPRESSION IN BOTH DIRECTIONS.

CC -!- SUBUNIT: MAY FORM A HETERODIMER WITH A RELATED FAMILY MEMBER.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear (Potential).
CC -!- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M34079; AAA36666.1; -.
CC EMBL; BC008713; AAH08713.1; -.
CC PIR; A34832; A34832.
CC Genew; HGNC:9549; PSMC3.
CC MIM: 186852; -.
CC InterPro; IPR003593; AAA_ATPase.
CC InterPro; IPR003959; AAA_ATPase_centri.
CC InterPro; IPR003960; AAA_sub.
CC Pfam; PF00004; AAA; 1.
CC SMART; SM00382; AAA; 1.
CC TIGRFAMs; TIGR01242; 26Sp45; 1.
CC PROSITE; PS00674; AAA; 1.
CC Proteasome; ATP-binding; Nuclear protein.
KW NP_BIND 227 234 ATP (POTENTIAL).
FT MUTAGEN 233 233 K->H: LOSS OF FUNCTION.
FT MUTAGEN 289 289 D->A: LOSS OF FUNCTION.
FT CONFLICT 409 409 R -> A (IN REF. 1 AND 3).
SQ SEQUENCE 439 AA; 49203 MW; 0E443465DDDEBB0B CRC64;

Query Match 61.4%; Score 35; DB 1; Length 439;
Best Local Similarity 50.0%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
DB 387 CTDDFNGAQC 396

RESULT 12
PRSA_RAT STANDARD; PRT; 439 AA.
AC Q63569; P97638;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 26S protease regulatory subunit 6A (Tat-binding protein 1) (TBP-1)
DE (Spermatogenic cell/sperm-associated Tat-binding protein homolog
DE SATA).
GN PSMC3 OR TBPI.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96183075; PubMed=8607789;
RA Makino Y., Yagosawa S., Kanemaki M., Yoshida T., Yamano K.,
RA Kishimoto T., Moncollin V., Egly J.M., Muramatsu M., Tamura T.;
RT "Structures of the rat proteasomal ATPases: determination of highly
RT conserved structural motifs and rules for their spacing."
RL Biochem. Biophys. Res. Commun. 220:1049-1054(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RX MEDLINE=97410049; PubMed=9266764;
RA Rivkin E., Cullinan E.B., Tres L.L., Kierszenbaum A.L.;
RT "A protein associated with the manchette during rat spermiogenesis is
RT encoded by a gene of the TBP-1-like subfamily with highly conserved
RT ATPase and protease domains."
RL Mol. Reprod. Dev. 48:77-89(1997).

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FT DOMAIN 301 341 EGF-LIKE 3.
FT DOMAIN 370 424 IG-LIKE C2-TYPE DOMAIN 2.
FT DOMAIN 444 536 FIBRONECTIN TYPE-III 1.
FT DOMAIN 541 632 FIBRONECTIN TYPE-III 2.
FT DOMAIN 638 732 FIBRONECTIN TYPE-III 3.
FT DOMAIN 824 1096 PROTEIN KINASE.
FT NP_BIND 830 838 ATP (BY SIMILARITY).
FT BINDING 855 855 ATP (BY SIMILARITY).
FT CARBOHYD 964 964 BY SIMILARITY.
FT CARBOHYD 140 140 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 399 399 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 464 464 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 560 560 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 596 596 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 691 691 N-LINKED (GLCNAC. .) (POTENTIAL).
FT MOD_RES 992 992 PHOSPHORYLATION (AUTO-).
FT VARIANT 849 849 R -> W (IN VMCM1; ACTIVATING EFFECT).
FT VARIANT 897 897 /FTID=VAR_006352.
FT VARIANT 897 897 Y -> S (IN VMCM1; ACTIVATING EFFECT).
FT VARIANT 897 897 /FTID=VAR_008716.
SQ SEQUENCE 1124 AA; 125810 MW; 658C05D18F4ACCEC CRC64;

Query Match 61.4%; Score 35; DB 1; Length 1124;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
DB 289 CATGWKGLQC 298

RESULT 14
TIE2_BOVIN
ID TIE2_BOVIN STANDARD; PRT; 1125 AA.
AC Q05807;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Angiopoietin 1 receptor precursor (BC 2.7.1.112) (Tyrosine-protein
kinase receptor TIE-2).
GN TEK OR TIE2 OR TIE-2.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Endothelial cells;
RX MEDLINE=94022374; Pubmed=8415706;
RA Sato T.N., Qin Y., Kozak C.A., Andrus K.L.;
RA "tie-1 and tie-2 define another class of putative receptor tyrosine
kinase genes expressed in early embryonic vascular system.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9355-9358(1993).
CC -1- FUNCTION: THIS PROTEIN IS A PROTEIN TYROSINE-KINASE TRANSMEMBRANE
RECEPTOR FOR ANGIOPOIETIN 1. IT MAY CONSTITUTE THE EARLIEST
MAMMALIAN ENDOTHELIAL CELL LINEAGE MARKER. PROBABLY REGULATES
ENDOTHELIAL CELL PROLIFERATION, DIFFERENTIATION AND GUIDES THE
PROPER PATTERNING OF ENDOTHELIAL CELLS DURING BLOOD VESSEL
FORMATION.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: SPECIFICALLY EXPRESSED IN DEVELOPING VASCULAR
ENDOTHELIAL CELLS.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. TIE
SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 EGF-LIKE DOMAINS.

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EMBL: X71424; CAA50555.1; -
PIR: S32691; S32691.
HSP: P11362; IFGK.
InterPro: IPR000561; EGF-like.
InterPro: IPR000719; Euk_pkinase.
InterPro: IPR003961; FN.III.
InterPro: IPR002049; Laminin_EGF.
InterPro: IPR001245; Tyr_pkinase.
Pfam: PF00008; EGF; 2.
Pfam: PF00041; fn3; 3.
Pfam: PF00069; pkinase; 1.
PRINTS: PR0109; TYRKINASE.
ProDom: PD000001; Euk_pkinase; 1.
SMART: SM00180; EGF_Lam; 1.
SMART: SM00001; EGF_like; 1.
SMART: SM00060; FN3; 3.
SMART: SM00219; TyRK; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00022; EGF_1; 3.
PROSITE: PS00022; EGF_2; 2.
Receptor; Tyrosine-protein kinase; Transferase; Signal; ATP-binding;
Repeat; EGF-like domain; Transmembrane; Immunoglobulin domain;
Glycoprotein; phosphorylation; Multigene family.
SIGNAL 1 18
CHAIN 19 1125 ANGIOPOIETIN 1 RECEPTOR.
DOMAIN 19 746 EXTRACELLULAR (POTENTIAL).
TRANSMEM 747 771 POTENTIAL.
DOMAIN 772 1125 CYTOPLASMIC (POTENTIAL).
DOMAIN 44 102 IG-LIKE C2-TYPE DOMAIN 1.
DOMAIN 210 252 EGF-LIKE 1.
DOMAIN 254 299 EGF-LIKE 2.
DOMAIN 301 341 EGF-LIKE 3.
DOMAIN 370 424 IG-LIKE C2-TYPE DOMAIN 2.
DOMAIN 444 538 FIBRONECTIN TYPE-III 1.
DOMAIN 541 635 FIBRONECTIN TYPE-III 2.
DOMAIN 639 730 FIBRONECTIN TYPE-III 3.
DOMAIN 825 1097 PROTEIN KINASE.
NP_BIND 831 839 ATP (BY SIMILARITY).
BINDING 856 856 ATP (BY SIMILARITY).
ACT_SITE 965 965 BY SIMILARITY.
MOD_RES 993 993 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).
SEQUENCE 1125 AA; 125927 MW; 015F1320A853B7F CRC64;

Query Match 61.4%; Score 35; DB 1; Length 1125;
Best Local Similarity 60.0%; Pred. No. 54;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
DB 289 CATGWKGLQC 298

RESULT 15
NGF_PIG
ID NGF_PIG STANDARD; PRT; 229 AA.
AC Q29074;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Beta-nerve growth factor precursor (Beta-NGF) (Fragment).
GN NGFB.

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OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Large white; TISSUE=Blood;
RX MEDLINE=94313891; PubMed=8039422;
RA Labib-Mansais Y., Mellink C., Verle M., Gellin J.;
RT "A new marker (NGFB) on pig chromosome 4, isolated by using a
RT consensus sequence conserved among species.";
RL Cytogenet. Cell Genet. 67:120-125(1994).
CC -!- FUNCTION: NERVE GROWTH FACTOR IS IMPORTANT FOR THE DEVELOPMENT AND
CC MAINTENANCE OF THE SYMPATHETIC AND SENSORY NERVOUS SYSTEMS. IT
CC STIMULATES DIVISION AND DIFFERENTIATION OF SYMPATHETIC AND
CC EMBRYONIC SENSORY NEURONS.
CC -!- SUBUNIT: HOMODIMER, ASSOCIATED BY NONCOVALENT FORCES.
CC -!- SIMILARITY: BELONGS TO THE NGF-BETA FAMILY.
CC -----
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CC -----
DR EMBL; L31898; AAA21301.1; -.
DR HSP; P01139; LBET.
DR InterPro; IPR002072; NGF.
DR Pfam; PF00243; NGF; 1.
DR ProDom; PD002052; NGF; 1.
DR SMART; SM00140; NGF; 1.
DR PROSITE; PS00248; NGF_1; 1.
DR PROSITE; PS0270; NGF_2; 1.
KW Growth factor; Signal.
FT NON_TER 1
FT SIGNAL <1 6
FT PROPEP 7
FT CHAIN 110 229
FT DISULFD 124 189
FT DISULFD 167 217
FT DISULFD 177 219
FT CARBOHYD 57 57
FT CARBOHYD 102 102
FT CARBOHYD 154 154
SQ SEQUENCE 229 AA; 25275 MW; FE8890771CBA3189 CRC64;
Query Match 59.6%; Score 34; DB 1; Length 229;
Best Local Similarity 87.5%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATDIKGA 9
DB 137 ATDIKGE 144

```

Search completed: November 9, 2002, 14:01:44
 Job time : 8.69231 secs

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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:34 ; Search time 13.8462 Seconds.
(without alignments)
69.430 Million cell updates/sec

Title: US-09-632-748-9

Perfect score: 57

Sequence: 1 CATDIKGAEC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	66.7	362	2 T42049	mom-2 protein - Ca
2	38	66.7	381	2 T34254	hypothetical prote
3	38	66.7	963	2 T09478	ubiquitin thiolest
4	38	66.7	2703	1 A24420	notch protein - fr
5	37	64.9	40	2 S20773	Ig heavy chain V r
6	35	61.4	118	1 PSLT3E	phospholipase A2 (
7	35	61.4	118	1 PSLT4E	phospholipase A2 (
8	35	61.4	118	1 PSLT1E	phospholipase A2 (
9	35	61.4	119	1 PS0XA	phospholipase A2 (
10	35	61.4	271	2 F95945	probable formimido
11	35	61.4	404	2 A34832	Tat-binding protei
12	35	61.4	430	2 T33155	hypothetical prote
13	35	61.4	939	2 T18974	hypothetical prote
14	35	61.4	965	2 T22933	hypothetical prote
15	35	61.4	1048	2 T04172	hypothetical prote
16	35	61.4	1124	1 F58388	Ca2+-transporting
17	35	61.4	1125	1 S57846	protein-tyrosine k
18	34.5	60.5	1456	2 T15961	protein-tyrosine k
19	34	59.6	103	2 S08462	hypothetical prote
20	34	59.6	125	2 A26312	Ig heavy chain V r
21	34	59.6	227	2 H71811	nerve growth facto
22	34	59.6	229	2 I46614	hypothetical prote
23	34	59.6	235	2 S14481	nerve growth facto
24	34	59.6	241	2 JL0097	nerve growth facto
25	34	59.6	243	2 A26311	nerve growth facto
26	34	59.6	245	2 I58570	beta-nerve growth
27	34	59.6	254	2 B55904	C 3.4.25.1 proteas
28	34	59.6	286	1 NGHUBM	nerve growth facto
29	34	59.6	289	2 D42586	glucuronosyltransf

glucuronosyltransf
glucuronosyltransf
sigma-B regulator
nerve growth facto
asparaginase (BC 3
probable cell grow
RNA 3'-terminal ph
probable cell grow
ATP-gated ionchann
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
protein Fl1C7.4 [1
estrogen receptor

ALIGNMENTS

RESULT 1

T42049

mom-2 protein - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000

C:Accession: T42049

R:Rocheleau, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; P
Cell 90, 707-716, 1997

A:Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans e
A:Reference number: Z15051; MUID:97433081; PMID:9288750

A:Accession: T42049

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-362 <ROC>

A:Cross-references: EMBL:AF013952; NID:q2343266; PIDN:AAC47749.1; PID:q2343267

C:Genetics:

A:Gene: mom-2

C:Superfamily: int-1 transforming protein

Query Match 66.7%; Score 38; DB 2; Length 362;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

||| ||| |||

Db 304 CATDVKDEEC 313

RESULT 2

T34254

hypothetical protein F38E1.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000

C:Accession: T34254

R:Gattung, S.; Le, T.

submitted to the EMBL Data Library, December 1995

A:Description: The sequence of C. elegans cosmid F38E1.

A:Reference number: Z21495

A:Accession: T34254

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-381 <GAT>

A:Cross-references: EMBL:U41996; PIDN:AAA83472.1; CESP:F38E1.7

C:Genetics:

A:Gene: CESP:F38E1.7

A:Introns: 26/2; 69/3; 105/1; 131/3; 288/3; 346/3

C:Superfamily: int-1 transforming protein

Query Match

66.7%; Score 38; DB 2; Length 381;

Best Local Similarity 60.0%; Pred. No. 16;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
||| :|||
Db 304 CAIDVKDREC 313

RESULT 3

T09478
ubiquitin thiolesterase (EC 3.1.2.15) - human
N:Alternate names: ubiquitin carboxy-terminal esterase
C:Species: Homo sapiens (man)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: T09478
R:Gray, D.A.
Submitted to the EMBL Data Library, October 1997
A:Reference number: Z16684
A:Accession: T09478
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-963 <GRA>
A:Cross-references: EMBL:U20657; NID:g2459396; PID:g2459395
C:Genetics:
A:Gene: Unph
A:Map position: 3
C:Keywords: proto-oncogene; thiolester hydrolase

Query Match 66.7%; Score 38; DB 2; Length 963;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
||| :|||
Db 568 CSTSVDSSEC 577

RESULT 4

A24420
notch protein - fruit fly (*Drosophila melanogaster*)
N:Alternate names: neurogenic repetitive locus protein
C:Species: *Drosophila melanogaster*
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A24420; S09358; A05267
R:Kidd, S.; Kelley, M.R.; Young, M.W.
Mol. Cell. Biol. 6, 3094-3108, 1986
A:Reference number: A24420; MUID:87064624; PMID:3097517
A:Accession: A24420
A:Molecule type: DNA
A:Residues: 1-2703 <KID>
A:Cross-references: GB:K03508; NID:gl57991; PIDN:AAA28725.1; PID:gl57993
R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Artavanis-Tsakonas, S.
Cell 43, 567-581, 1985
A:Reference number: A24768; MUID:86079539; PMID:3935325
A:Accession: A24768
A:Molecule type: mRNA
A:Residues: 1-48, 'I', 50-110, 'R', 120-230, 'I', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958
A:Note: the authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
R:Tautz, D.

Nucleic Acids Res. 17, 6463-6471, 1989
A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA markers
A:Reference number: S09358; MUID:89385974; PMID:2780284
A:Accession: S09358
A:Molecule type: DNA
A:Residues: 2505-2551, 'QQQQ', 2552-2576, 'E', 2578-2604 <TAU>
R:Wharton, K.A.; Vedvobnick, B.; Finnerty, V.G.; Artavanis-Tsakonas, S.
Cell 40, 55-62, 1985
A:Title: opa: a novel family of transcribed repeats shared by the Notch locus and other
A:Reference number: A05267; MUID:85099329; PMID:2981631
A:Accession: A05267
A:Molecule type: DNA
A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>
C:Genetics:

A:Gene: notch; opa
A:Cross-references: FlyBase:FBgn0004647
A:Map position: 8.96-9.36

A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
C:Keywords: differentiation; tandem repeat; transmembrane protein
F:27-43/Domain: transmembrane #status predicted <TMM1>
F:297-328/Domain: EGF homology <EGX1>
F:530-561/Domain: EGF homology <EGF1>
F:568-599/Domain: EGF homology <EGF>
F:988-1019/Domain: EGF homology <EGX2>
F:1064-1095/Domain: EGF homology <EGX3>
F:1187-1218/Domain: transmembrane #status predicted <TMM2>
F:1746-1762/Domain: ankyrin repeat homology <AN1>
F:1950-1982/Domain: ankyrin repeat homology <AN2>
F:1983-2015/Domain: transmembrane #status predicted <TMM3>
F:2017-2049/Domain: ankyrin repeat homology <AN3>
F:2050-2082/Domain: ankyrin repeat homology <AN4>
F:2083-2115/Domain: ankyrin repeat homology <AN5>
F:2538-2568/Region: glutamine-rich
F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 66.7%; Score 38; DB 1; Length 2703;
Best Local Similarity 60.0%; Pred. No. 88;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
||| ||| :||
Db 437 CATGYKGVDC 446

RESULT 5

S20773
Ig heavy chain V region (VH3, IN48P1) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 19-Apr-1996 #text_change 23-Jul-1999
C:Accession: S20773
R:Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A:Description: Analysis of human cord blood Ig heavy chain IgA and IgG repertoire.
A:Reference number: S20764
A:Accession: S20773
A:Molecule type: DNA
A:Residues: 1-40 <MOR>
A:Cross-references: EMBL:Z11944; NID:g33878; PIDN:CAA78001.1; PID:g33879
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 64.9%; Score 37; DB 2; Length 40;
Best Local Similarity 60.0%; Pred. No. 3.4;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
||| :|||
Db 8 CTTDLGGAYC 17

RESULT 6

PSLT3E
phospholipase A2 (EC 3.1.1.4) III - broad-banded blue sea krait
N:Alternate names: phosphatidylcholine 2-acylhydrolase
C:Species: Laticauda semifasciata (broad-banded blue sea krait, erabu sea snake)
C:Date: 02-Apr-1982 #sequence_revision 13-Jun-1983 #text_change 28-Feb-1997
C:Accession: A00753
R:Nishida, S.; Kim, H.S.; Tamiya, N.
Biochem. J. 207, 589-594, 1982
A:Title: Amino acid sequences of three phospholipases A I, III and IV from the venom
A:Reference number: A90316; MUID:83153048; PMID:7165712
A:Accession: A00753
A:Molecule type: protein
A:Residues: 1-118 <NIS>
C:Function:
A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac
A:Note: the reaction is strongly enhanced when the phospholipid is condensed into a m
C:Superfamily: phospholipase A2

C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres
F;4,67/Binding site: micellar substrate (Gln, Tyr) #status predicted
F;11,27,117,29-45,44-98,51-91,60-84,78-89/Disulfide bonds: #status predicted
F;28,30,32,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F;48,92/Active site: His, Asp #status predicted

Query Match 61.4%; Score 35; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

||| : : :
Db 89 CACDLEAAKC 98

RESULT 7

PSLT4E

phospholipase A2 (EC 3.1.1.4) IV - broad-banded blue sea krait

N;Alternate names: phosphatidylcholine 2-acylhydrolase

C;Species: Laticauda semifasciata (broad-banded blue sea krait, erabu sea snake)

C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 28-Feb-1997

C;Accession: A90316; A00753

R;Nishida, S.; Kim, H.S.; Tamiya, N.

Biochem. J. 207, 589-594, 1982

A;Title: Amino acid sequences of three phospholipases A I, III and IV from the venom of

A;Reference number: A90316; MUID:83153048; PMID:7165712

A;Accession: A90316

A;Molecule type: protein

A;Residues: 1-118 <NIS>

A;Function:

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle

C;Superfamily: phospholipase A2

C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres

F;4,67/Binding site: micellar substrate (Gln, Tyr) #status predicted

F;11,27,117,29-45,44-98,51-91,60-84,78-89/Disulfide bonds: #status predicted

F;28,30,32,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F;48,92/Active site: His, Asp #status predicted

Query Match 61.4%; Score 35; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

||| : : :
Db 89 CACDLEAAKC 98

RESULT 8

PSLT4E

phospholipase A2 (EC 3.1.1.4) I - broad-banded blue sea krait

N;Alternate names: phosphatidylcholine 2-acylhydrolase

C;Species: Laticauda semifasciata (broad-banded blue sea krait, erabu sea snake)

C;Date: 02-Apr-1982 #sequence_revision 31-Dec-1989 #text_change 28-Feb-1997

C;Accession: A94325; A00752; A30821

R;Takasaki, C.; Kuramochi, H.; Shimazu, T.; Tamiya, N.

Toxicol. 26, 747-749, 1988

A;Title: Correction of amino acid sequence of phospholipase A-2 I from the venom of Laticauda semifasciata

A;Reference number: A94325; MUID:89044898; PMID:3188064

A;Accession: A94325

A;Molecule type: protein

A;Residues: 1-118 <TAK>

R;Nishida, S.; Kim, H.S.; Tamiya, N.

Biochem. J. 207, 589-594, 1982

A;Title: Amino acid sequences of three phospholipases A I, III and IV from the venom of

A;Reference number: A90316; MUID:83153048; PMID:7165712

A;Contents: annotation; specific activity

A;Note: Trp-64 is important to enzyme activity

C;Function:

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle

C;Superfamily: phospholipase A2

C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres

F;4,67/Binding site: micellar substrate (Gln, Tyr) #status predicted
F;11,27,117,29-45,44-98,51-91,60-84,78-89/Disulfide bonds: #status predicted
F;28,30,32,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted
F;48,92/Active site: His, Asp #status predicted

Query Match 61.4%; Score 35; DB 1; Length 118;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

||| : : :
Db 89 CACDLEAAKC 98

RESULT 9

PSOXA

phospholipase A2 (EC 3.1.1.4) taipoxin alpha chain - Australian taipan

N;Alternate names: phosphatidylcholine 2-acylhydrolase

C;Species: Oxyuranus scutellatus scutellatus (Australian taipan)

C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 28-Feb-1997

C;Accession: A00754

R;Lind, P.; Eaker, D.

Eur. J. Biochem. 124, 441-447, 1982

A;Title: Amino acid sequence of the alpha-subunit of taipoxin, an extremely potent pr
A;Reference number: A00754; MUID:82261658; PMID:7049694

A;Accession: A00754

A;Molecule type: protein

A;Residues: 1-119 <LIN>

C;Function:

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-ac
A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a m
C;Superfamily: phospholipase A2

C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; p

F;4,68/Binding site: micellar substrate (Gln, Tyr) #status predicted

F;11,72,27-118,29-45,44-99,51-92,61-85,79-90/Disulfide bonds: #status predicted

F;28,30,32,49/Binding site: calcium (Tyr, Gly, Asp) #status predicted

F;48,93/Active site: His, Asp #status predicted

Query Match 61.4%; Score 35; DB 1; Length 119;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

||| : : :
Db 90 CRCDAKAAEC 99

RESULT 10

F95945

probable formimidoylglutamate (EC 3.5.3.8) [imported] - Sinorhizobium meliloti (strai
C;Species: Sinorhizobium meliloti

C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 03-Jun-2002

C;Accession: F95945

R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Her

Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001

A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing e

A;Reference number: A95842; MUID:21396508; PMID:11481431

A;Accession: F95945

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-271 <KUR>

A;Cross-references: GB:AL591985; PIDN:CAC49230.1; PID:gl5140716; GSPDB:GN00167
A;Experimental source: strain 1021, megaplasmid pSymB

R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubl

Pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.

L.; Hyman, R.W.; Jones, T.

Science 293, 668-672, 2001

A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lalau

hebaul, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh,

A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.

A;Reference number: A96039; MUID:21368234; PMID:11474104

A;Contents: annotation

C;Genetics:

A:Gene: hutG; Smb21164
A:Genome: plasmid
C:Superfamily: Yersinia pestis hypothetical protein hutG
C:Keywords: hydrolase

Query Match 61.4%; Score 35; DB 2; Length 271;
Best Local Similarity 44.4%; Pred. No. 44;
Matches 8; Conservative 2; Mismatches 0; Indels 8; Gaps 1;

QY 1 CATDIK-----GAEC 10
|||||
Db 174 CATEIERAAETAGAAC 191

RESULT 11

A34832
Tat-binding protein-1 - human
C:Species: Homo sapiens (man)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 19-Jan-2001
C:Accession: A34832
R.Nelbock, P.; Dillon, P.J.; Perkins, A.; Rosen, C.A.
Science 248, 1650-1653, 1990
A:Title: A cDNA for a protein that interacts with the human immunodeficiency virus tat
A:Reference number: A34832; MUID:90302011; PMID:2194290
A:Accession: A34832
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-404 <NEL>
A:Cross-references: GB:M34079; NID:g338699; PIDN:AAA36666.1; PID:g338700
C:Superfamily: ATP-dependent 26S proteinase; Ftsh/SEC18/CDC48-type ATP-binding domain hc
C:Keywords: ATP; nucleotide binding; P-loop
F:165-375/Domain: Ftsh/SEC18/CDC48-type ATP-binding domain homology <VATP>
F:192-199/Region: nucleotide-binding motif A (P-loop)

Query Match 61.4%; Score 35; DB 2; Length 404;
Best Local Similarity 50.0%; Pred. No. 62;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
| | | | |
Db 352 CTDDFNGAQC 361

RESULT 12

T33155
hypothetical protein F56H1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Jan-2000
C:Accession: T33155
R.Graves, T.
submitted to the EMBL Data Library, May 1998
A:Description: The sequence of C. elegans cosmid F56H1.
A:Reference number: Z21293
A:Accession: T33155
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-430 <GRA>
A:Cross-references: EMBL:AF067618; PIDN:AAC19196.1; GSPDB:GN000019; CESP:F56H1.4
A:Experimental source: strain Bristol N2; clone F56H1
C:Genetics:
A:Gene: CESP:F56H1.4
A:Map position: 1
A:Introns: 221/1; 318/3; 367/2
C:Superfamily: ATP-dependent 26S proteinase; Ftsh/SEC18/CDC48-type ATP-binding domain hc

Query Match 61.4%; Score 35; DB 2; Length 430;
Best Local Similarity 50.0%; Pred. No. 66;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
| | | | |
Db 378 CTDDFNGAQC 387

RESULT 13

T18974
hypothetical protein C06A1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18974
R.McMurray, A.
submitted to the EMBL Data Library, June 1995
A:Reference number: Z19054
A:Accession: T18974
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-939 <WIL>
A:Cross-references: EMBL:Z49886; PIDN:CAA90054.1; GSPDB:GN000020; CESP:C06A1.4
A:Experimental source: clone C06A1
C:Genetics:
A:Gene: CESP:C06A1.4
A:Map position: 2
A:Introns: 52/3; 116/2; 146/3; 282/1; 524/2; 583/1; 639/2; 697/3; 779/3; 901/2

Query Match 61.4%; Score 35; DB 2; Length 939;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
| | | | |
Db 317 CAAVIKGLDC 326

RESULT 14

T22933
hypothetical protein F58G1.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T22933
R.Smyle, R.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19639
A:Accession: T22933
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-965 <WIL>
A:Cross-references: EMBL:Z81556; PIDN:CAB04524.1; GSPDB:GN000020; CESP:F58G1.1
A:Experimental source: clone F58G1
C:Genetics:
A:Gene: CESP:F58G1.1
A:Map position: 2
A:Introns: 52/3; 116/2; 172/3; 308/1; 550/2; 609/1; 665/2; 723/3; 805/3; 927/2

Query Match 61.4%; Score 35; DB 2; Length 965;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
| | | | |
Db 343 CAAVIKGLDC 352

RESULT 15

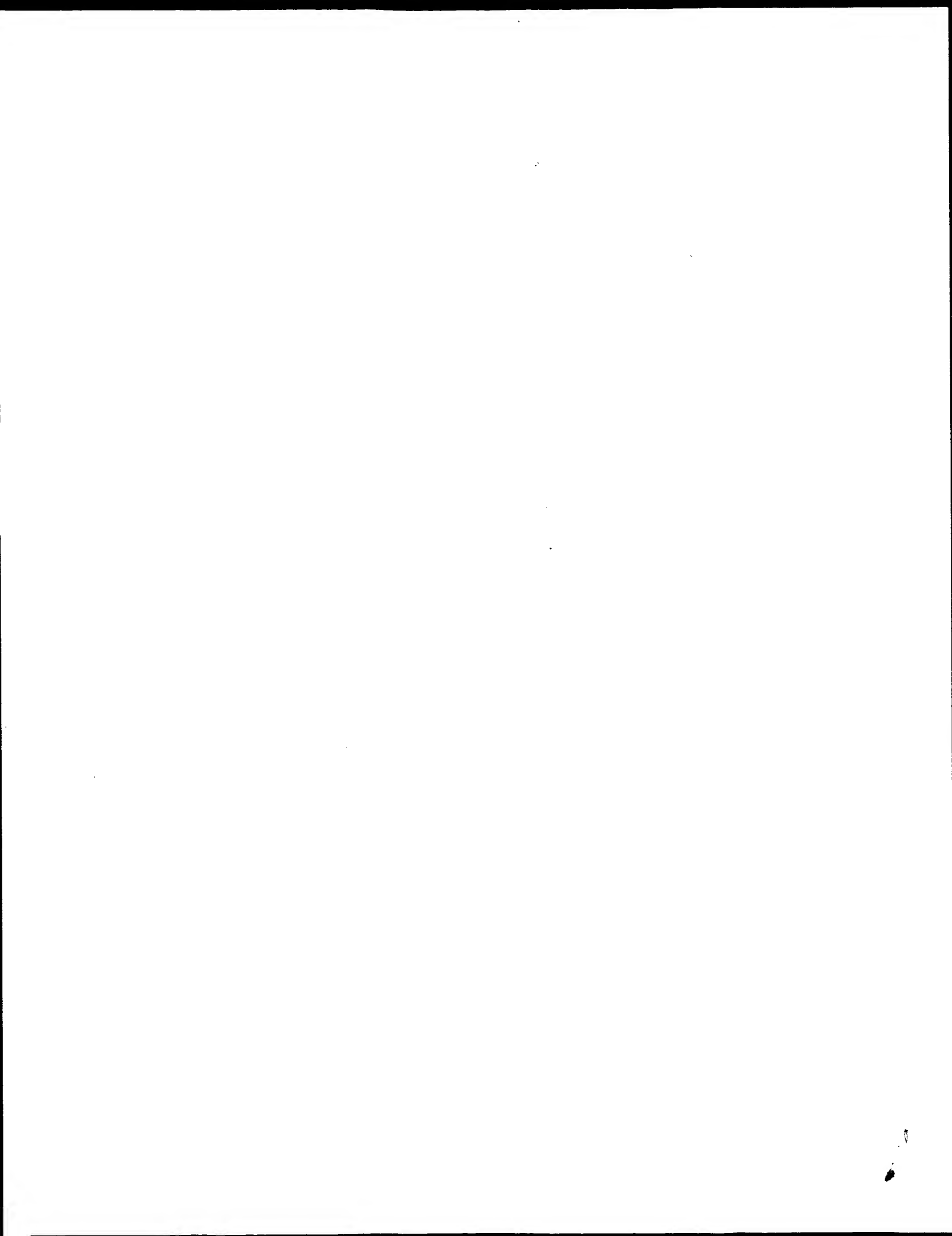
T04172
Ca2+-transporting ATPase (EC 3.6.3.8) - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 19-Apr-2002
C:Accession: T04172
R.Chen, X.; Chang, M.; Wang, B.; Wu, B.
Plant J. 11, 363-371, 1997
A:Title: Cloning of a Ca(2+)-ATPase gene and the role of cytosolic Ca2+ in the giber
A:Reference number: Z15255; MUID:9726952; PMID:9107028
A:Accession: T04172
A:Status: translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1048 <CHE>

A;Cross-references: EMBL:U82966; NID:g2160711; PIDN:AAB58910.1; PID:g2160712
 A;Experimental source: cv.IR36
 C;Genetics:
 A;Introns: 444/3; 521/3; 615/3; 729/3; 779/3; 854/3
 C;Superfamily: Na+/K+-transporting ATPase alpha chain; ATPase nucleotide-binding domain
 C;Keywords: hydrolase; phosphoprotein
 F;39-56/Domain: calcium binding #status predicted <CA1>
 F;106-130/Domain: calcium binding #status predicted <CA2>
 F;236-256/Domain: calcium binding #status predicted <CA3>
 F;317-336/Domain: calcium binding #status predicted <CA4>
 F;513-696/Domain: ATP binding #status predicted <ATP>
 F;610-784/Domain: ATPase nucleotide-binding domain homology <ATN>
 F;755-776/Domain: calcium binding #status predicted <CA5>
 F;358/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 61.4%; Score 35; DB 2; Length 1048;
 Best Local Similarity 75.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TDIKGAC 10
 |||:| |
 Db 197 TDIQKEC 204

Search completed: November 9, 2002, 14:03:43
 Job time : 14.8462 secs



GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2002, 14:03:09 ; Search time 6.15385 Seconds
(without alignments)
23.430 Million cell updates/sec

Title: US-09-632-748-9

Perfect score: 57

Sequence: 1 CATDIKGAEC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	59.6	72	10	US-09-848-664-21
2	34	59.6	121	12	US-10-072-681-2
3	34	59.6	121	12	US-10-072-681-3
4	34	59.6	142	8	US-08-450-842-52
5	34	59.6	153	10	US-09-798-338-2
6	34	59.6	157	10	US-09-798-338-4
7	34	59.6	163	10	US-09-798-338-6
8	34	59.6	167	10	US-09-798-338-8
9	34	59.6	241	8	US-08-450-842-5
10	34	59.6	241	10	US-09-822-263-16
11	34	59.6	242	12	US-10-072-681-1
12	34	59.6	289	10	US-09-305-856B-4
13	34	59.6	289	10	US-09-305-856B-6
14	34	59.6	289	10	US-09-305-856B-8
15	34	59.6	373	10	US-09-919-497-53
16	33	57.9	60	10	US-09-864-761-40315
17	33	57.9	365	10	US-09-815-242-11521
18	33	57.9	2724	9	US-09-808-602-13
19	33	57.9	2733	9	US-09-808-602-8

20	33	57.9	2764	9	US-09-808-602-80	Sequence 80, Appl
21	33	57.9	2765	9	US-09-808-602-84	Sequence 84, Appl
22	33	57.9	2771	9	US-09-808-602-82	Sequence 82, Appl
23	32	56.1	32	12	US-10-001-843-149	Sequence 149, App
24	32	56.1	65	10	US-09-864-761-46197	Sequence 46197, A
25	32	56.1	223	12	US-10-036-342-61	Sequence 61, Appl
26	32	56.1	227	12	US-10-003-152-2	Sequence 2, Appl
27	31	54.4	66	10	US-09-864-761-40020	Sequence 40020, A
28	31	54.4	234	10	US-09-915-593-2	Sequence 2, Appl
29	31	54.4	241	10	US-09-915-593-28	Sequence 28, Appl
30	31	54.4	241	12	US-10-116-378-3	Sequence 3, Appl
31	31	54.4	317	12	US-10-116-378-26	Sequence 26, Appl
32	31	54.4	454	10	US-09-815-242-11157	Sequence 11157, A
33	31	54.4	619	10	US-09-764-870-308	Sequence 308, App
34	31	54.4	3635	10	US-09-845-583-2	Sequence 2, Appl
35	31	54.4	4679	10	US-09-804-898-2	Sequence 2, Appl
36	31	54.4	5701	10	US-09-864-761-37319	Sequence 37319, A
37	30.5	53.5	129	10	US-09-864-761-47279	Sequence 47279, A
38	30	52.6	8	10	US-09-866-898-2	Sequence 2, Appl
39	30	52.6	80	10	US-09-804-156-38	Sequence 38, Appl
40	30	52.6	168	10	US-09-864-761-40976	Sequence 40976, A
41	30	52.6	289	10	US-09-919-497-54	Sequence 54, Appl
42	30	52.6	318	10	US-09-886-055-55	Sequence 55, Appl
43	30	52.6	355	9	US-09-947-953-2	Sequence 2, Appl
44	30	52.6	450	10	US-09-826-752-2	Sequence 2, Appl
45	30	52.6	472	10	US-09-815-242-11137	Sequence 11137, A

ALIGNMENTS

RESULT 1
US-09-848-664-21
; Sequence 21, Application US/09848664
; Patent No. US20020146414A1
; GENERAL INFORMATION:
; APPLICANT: Sakiyama-Elbert, Shelly E.
; APPLICANT: Hubbell, Jeffrey A.
; TITLE OF INVENTION: Controlled Release of No. US20020146414A1-Heparin Binding Grow
; TITLE OF INVENTION: Factors from Heparin Containing Matrices
; FILE REFERENCE: ETH 108
; CURRENT APPLICATION NUMBER: US/09/848,664
; PRIOR FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: 09/298,084
; PRIOR FILING DATE: 1999-04-22
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 21
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-848-664-21

Query Match 59.6%; Score 34; DB 10; Length 72;
Best Local Similarity 87.5%; Pred No. 6.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGAEC 9

DB 28 ATDIKGAEC 35

RESULT 2

US-10-072-681-2
; Sequence 2, Application US/10072681
; Patent No. US20020137893A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmelzer, Charles H.
; APPLICANT: Beck, Joanne T.
; TITLE OF INVENTION: PURIFICATION OF NGF
; FILE REFERENCE: GENENT 037C3
; CURRENT APPLICATION NUMBER: US/10/072,681

```
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/675,503
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-072-681-2
Query Match      59.6%; Score 34; DB 12; Length 121;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATDIKGA 9
Db 29 ATDIKGE 36

RESULT 3
US-10-072-681-3
; Sequence 3, Application US/10072681
; Patent No. US20020137893A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Beck, Joanne T.
; TITLE OF INVENTION: PURIFICATION OF NGF
; FILE REFERENCE: GENE.037C3
; CURRENT APPLICATION NUMBER: US/10/072,681
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/675,503
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 121
; TYPE: PRT
; ORGANISM: mouse
US-10-072-681-3
Query Match      59.6%; Score 34; DB 12; Length 121;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATDIKGA 9
Db 29 ATDIKGE 36

RESULT 4
US-08-450-842-52
; Sequence 52, Application US/08450842
; Patent No. US20020045576A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
```

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; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,842
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/426419
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030013
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 666P2C1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 142 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-842-52
Query Match      59.6%; Score 34; DB 8; Length 142;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ATDIKGA 9
Db 28 ATDIKGE 35

RESULT 5
US-09-798-338-2
; Sequence 2, Application US/09798338
; Patent No. US20010020086A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Schense, Jason C.
; APPLICANT: Sakiyama, Shelly E.
; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
; FILE REFERENCE: 87662-68879
; CURRENT APPLICATION NUMBER: US/09/798,338
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/141,153
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
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; LENGTH: 153
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificial
US-09-798-338-2
; OTHER INFORMATION: Protein Sequence

Query Match          59.6%; Score 34; DB 10; Length 153;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 ATDIKGAE 9
Db   62 ATDIKGKE 69

RESULT 6
US-09-798-338-4
; Sequence 4, Application US/09798338
; Patent No. US20010020086A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Schense, Jason C.
; APPLICANT: Sakiyama, Shelly E.
; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
; FILE REFERENCE: 87662-68879
; CURRENT APPLICATION NUMBER: US/09/798,338
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/141,153
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificial
US-09-798-338-4
; OTHER INFORMATION: Protein Sequence

Query Match          59.6%; Score 34; DB 10; Length 157;
Best Local Similarity 87.5%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 ATDIKGAE 9
Db   66 ATDIKGKE 73

RESULT 7
US-09-798-338-6
; Sequence 6, Application US/09798338
; Patent No. US20010020086A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Schense, Jason C.
; APPLICANT: Sakiyama, Shelly E.
; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
; FILE REFERENCE: 87662-68879
; CURRENT APPLICATION NUMBER: US/09/798,338
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/141,153
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 163
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificial
US-09-798-338-6
; OTHER INFORMATION: Protein Sequence

Query Match          59.6%; Score 34; DB 10; Length 163;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 ATDIKGAE 9
Db   72 ATDIKGKE 79

RESULT 8
US-09-798-338-8
; Sequence 8, Application US/09798338
; Patent No. US20010020086A1
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Schense, Jason C.
; APPLICANT: Sakiyama, Shelly E.
; TITLE OF INVENTION: ENZYME-MEDIATED MODIFICATION OF FIBRIN FOR TISSUE
; FILE REFERENCE: 87662-68879
; CURRENT APPLICATION NUMBER: US/09/798,338
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/141,153
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Artificial
US-09-798-338-8
; OTHER INFORMATION: Protein Sequence

Query Match          59.6%; Score 34; DB 10; Length 167;
Best Local Similarity 87.5%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY  2 ATDIKGAE 9
Db   76 ATDIKGKE 83

RESULT 9
US-08-450-842-5
; Sequence 5, Application US/08450842
; Patent No. US20020045576A1
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: ROSENTHAL, ARNON
; TITLE OF INVENTION: NOVEL NEUROTROPHIC FACTOR
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/450,842
; FILING DATE:
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; CLASSIFICATION: 514
; PRIOR APPLICATION DATA: 08/426419
; FILING DATE: 19-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/030013
; FILING DATE: 22-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648482
; FILING DATE: 31-JAN
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/587707
; FILING DATE: 1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: 666P2C1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8674
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 241 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-450-842-5

Query Match 59.6%; Score 34; DB 8; Length 241;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
DB 149 ATDIKGE 156

RESULT 10
US-09-822-263-16
; Sequence 16, Application US/09822263
; Patent No. US20020036598A1
; GENERAL INFORMATION:
; APPLICANT: Prayaga, Sudhirdas
; APPLICANT: Vernet, Corine
; APPLICANT: Shimkets, Richard A
; APPLICANT: Burgess, Catherine
; APPLICANT: Spytek, Kimberly
; APPLICANT: Tchernev, Velizar T
; TITLE OF INVENTION: No. US20020036598A1el Polynucleotides and Polypeptides Encoded Th
; FILE REFERENCE: 15966-572 CIP1
; CURRENT APPLICATION NUMBER: US/09/822,263
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 09/672,665
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/156,745
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 60/158,942
; PRIOR FILING DATE: 1999-10-06
; PRIOR APPLICATION NUMBER: 60/159,248
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/169,344
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 60/215,048
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-822-263-16

Query Match 59.6%; Score 34; DB 10; Length 241;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
DB 149 ATDIKGE 156

RESULT 11
US-10-072-681-1
; Sequence 1, Application US/10072681
; Patent No. US20020137893A1
; GENERAL INFORMATION:
; APPLICANT: Burton, Louis E.
; APPLICANT: Schmelzer, Charles H.
; APPLICANT: Beck, Joanne T.
; TITLE OF INVENTION: PURIFICATION OF NGF
; FILE REFERENCE: GENENT.037C3
; CURRENT APPLICATION NUMBER: US/10/072,681
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 60/030838
; PRIOR FILING DATE: 1996-11-15
; PRIOR APPLICATION NUMBER: 60/047855
; PRIOR FILING DATE: 1997-05-29
; PRIOR APPLICATION NUMBER: 08/970865
; PRIOR FILING DATE: 1997-11-14
; PRIOR APPLICATION NUMBER: 09/363573
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: 09/675,503
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-072-681-1

Query Match 59.6%; Score 34; DB 12; Length 242;
Best Local Similarity 87.5%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
DB 150 ATDIKGE 157

RESULT 12
US-09-305-856B-4
; Sequence 4, Application US/09305856B
; Patent No. US20020061518A1
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; TITLE OF INVENTION: Genotyping the Human
; FILE REFERENCE: 4389-7 (formerly SEQ-17CIP)
; CURRENT APPLICATION NUMBER: US/09/305,856B
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 60/084,807
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-305-856B-4

Query Match 59.6%; Score 34; DB 10; Length 289;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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DR WPI; 1999-121938/11.
 XX Peptides containing amino acid sequence GA - useful for inhibiting
 PT amyloid formation and associated cytotoxicity in the treatment of
 PT type II diabetes mellitus
 XX
 XX Claim 5; Column 5; 8pp; German.
 PS
 XX This invention describes novel agonists (competitive inhibitor) and/or
 CC inhibitors of amyloid formation peptides which are 3-15 amino acids in
 CC length and contain at least the active sequence GA. The new peptides
 CC are useful for inhibiting amyloid formation and associated cytotoxicity
 CC in the treatment of type II diabetes mellitus, Alzheimer's disease and
 CC spongiform encephalopathies (e.g. CJD, scrapie and BSE).
 XX
 XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 15; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 Db 4 KGA 6

RESULT 45
 AAW93022
 ID AAW93022 standard; peptide; 8 AA.
 XX
 AC AAW93022;
 XX
 DT 18-MAY-1999 (first entry)
 XX
 DE DE19725619 peptide #13.
 XX
 KW Agonist; cytotoxic; competitive inhibitor; amyloid formation; treatment;
 KW type II diabetes mellitus; Alzheimer's disease; CJD; scrapie; BSE;
 KW spongiform encephalopathy.
 XX
 OS Synthetic.
 XX
 PN DE19725619-Al.
 XX
 PD 24-DEC-1998.
 XX
 PF 17-JUN-1997; 97DE-1025619.
 XX
 PR 17-JUN-1997; 97DE-1025619.
 XX
 PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX
 PI Bernhagen J, Brunner H, Kapurniotu A;
 XX
 DR WPI; 1999-121938/11.
 XX
 PT Peptides containing amino acid sequence GA - useful for inhibiting
 PT amyloid formation and associated cytotoxicity in the treatment of
 PT type II diabetes mellitus
 XX
 PS Claim 5; Column 5; 8pp; German.
 XX
 XX This invention describes novel agonists (competitive inhibitor) and/or
 CC inhibitors of amyloid formation peptides which are 3-15 amino acids in
 CC length and contain at least the active sequence GA. The new peptides
 CC are useful for inhibiting amyloid formation and associated cytotoxicity
 CC in the treatment of type II diabetes mellitus, Alzheimer's disease and
 CC spongiform encephalopathies (e.g. CJD, scrapie and BSE).
 XX
 XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 15; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 Db 2 KGA 4
 Search completed: November 9, 2002, 14:12:36
 Job time : 36 secs

PN WO9808874-A1.
 XX 05-MAR-1998.
 PD
 XX 27-AUG-1997; 97WO-US15167.
 PF
 XX 27-AUG-1996; 96US-0025799.
 PR
 XX (CHIR) CHIRON CORP.
 PA
 XX Granoff D, Moe GR;
 PI
 XX WPI; 1998-216938/19.
 DR
 XX Antibodies to *Neisseria meningitidis* serotype B - prepared using
 PT capsular polysaccharide derivatives, used to develop products for
 PT treating or preventing infections, e.g. meningitis and sepsis
 XX
 PS Claim 17; Fig 7A; 109pp; English.
 XX
 CC This sequence represents a molecular mimetic of a unique epitope of
 CC *Neisseria meningitidis* serotype B (MenB). This sequence was isolated
 CC using the antibodies (Ab) of the invention. The Ab are directed against
 CC a MenB capsular polysaccharide (PS) derivative, and are not autoreactive.
 CC The Ab either do not cross-react or they are minimally cross-reactive.
 CC with host tissues and therefore pose minimal risk of evoking immune
 CC disease. The non-autoreactive Ab are particularly useful for identifying
 CC molecular mimetics of unique MenB PS epitopes that can be used in vaccine
 CC compositions. Furthermore, the Ab, humanised versions of the Ab,
 CC fragments and functional equivalents, will also find use in passive
 CC immunisation against, and/or as an adjunct to therapy for, MenB and
 CC *Escherichia coli* K1 disease. Such disease includes bacterial meningitis
 CC and sepsis in infants, children and adults. The anti-MenB Ab can also be
 CC used to investigate the bactericidal and/or opsonic function of Ab of
 CC different specificities, as well as to identify the molecular nature of
 CC the unique epitopes on the MenB bacterial surface that are not
 CC cross-reactive with host PS. The anti-MenB Ab can be used to isolated
 CC fractions of MenB bacteria or MenB PS derivatives. Once isolated, the
 CC critical epitopes reactive with the anti-MenB Ab can be characterised and
 CC employed directly in oligosaccharide protein conjugate vaccines or to
 CC model synthetic saccharides or mimetics for use in vaccines.
 CC
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 15; DB 19; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 3 KGA 5
 XX
 RESULT 43
 AAY39236
 ID AAY39236 standard; peptide; 8 AA.
 XX
 AC AAY39236;
 KW
 XX 23-NOV-1999 (first entry)
 DT
 DE Beta-amyloid fragment for generation of p75NTR inhibiting peptides.
 XX
 KW p75NTR; p75 neurotrophin receptor; nerve growth factor;
 KW NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid fragment;
 KW Alzheimer's disease; pseudo-ligand; hair growth; hair colour;
 KW skin colour; alopecia areata; male pattern baldness.
 XX
 OS Synthetic.
 XX
 XX WO9939728-A2.
 PN
 XX 12-AUG-1999.
 PD

XX 03-FEB-1999; 99WO-US02362.
 PF
 XX 04-FEB-1998; 98US-0018194.
 PR
 XX (UYBO-) UNIV BOSTON.
 PA
 XX Eller M, Gilchrist BA, Yaar M;
 PI
 XX WPI; 1999-539950/45.
 DR
 XX Controlling or manipulating melanocyte and keratinocyte cell death,
 PT useful for treating, e.g. alopecia areata
 PT
 XX Disclosure; Page 15; 67pp; English.
 PS
 XX This sequence is amino acids 24-31 of beta-amyloid. This sequence can be
 CC used to generate cyclic peptide AAY39233. The cyclic peptide competes
 CC with and competitively inhibits beta-amyloid binding to the p75
 CC neurotrophin receptor (p75NTR). p75NTR is a low affinity nerve growth
 CC factor (NGF) receptor which is expressed by melanocytes and keratinocytes
 CC of the basal epidermis. Apoptosis can be inhibited by p75NTR via the
 CC upregulation of the Bcl-2 protein. If the receptor is occupied by
 CC appropriate ligands e.g. neurotrophins, apoptosis is inhibited. Other
 CC examples of appropriate ligands include this cyclic peptide. This peptide
 CC is based on the sequence of the binding fragment of beta-amyloid, which
 CC binds to p75NTR in Alzheimer's disease. This cyclic peptide can be used
 CC in methods to control or manipulate keratinocyte or melanocyte cell
 CC death. The methods involve using this peptide or peptides AAY39234-Y39235
 CC to bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting
 CC apoptosis. The new method can induce or maintain hair growth, hair colour
 CC or skin colour. Inducing or maintaining hair growth is useful for
 CC treating alopecia areata or male pattern baldness in vertebrates.
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 15; DB 20; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 5 KGA 7
 XX
 RESULT 44
 AAW93021
 ID AAW93021 standard; peptide; 8 AA.
 XX
 AC AAW93021;
 KW
 XX 18-MAY-1999 (first entry)
 DT
 DE DE19725619 peptide #12.
 XX
 KW Agonist; cytotoxic; competitive inhibitor; amyloid formation; treatment;
 KW type II diabetes mellitus; Alzheimer's disease; CJD; scrapie; BSE;
 KW spongiform encephalopathy.
 KW
 OS Synthetic.
 XX
 PN DE19725619-A1.
 XX
 PD 24-DEC-1998.
 XX
 PF 17-JUN-1997; 97DE-1025619.
 XX
 XX 17-JUN-1997; 97DE-1025619.
 PR
 XX (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 PA
 XX Bernhagen J, Brunner H, Kapurniotu A;
 PI
 XX

RESULT 40
 AAW07226
 ID AAW07226 standard; peptide; 8 AA.
 XX
 AC AAW07226;
 DT 09-APR-1997 (first entry)
 XX
 DE HIV-1 group O strain DUR peptide (13) derived from gp120 V3 loop.
 XX
 KW Human immunodeficiency virus; subgroup; strain; AIDS; homology; envelop;
 KW gp120; gp41; seropositive; antibody; primer; probe; group O; group M.
 XX
 OS Human immunodeficiency virus type 1.
 XX
 PN WO9612809-A2.
 XX
 PD 02-MAY-1996.
 XX
 PF 20-OCT-1995; 95WO-FR01391.
 XX
 PR 03-MAR-1995; 95FR-0002526.
 PR 20-OCT-1994; 94FR-0012554.
 XX
 PA (INSP) INST PASTEUR.
 XX
 PI Borman A, Charneau P, Clavel F, Cohen JHM, Guetard D;
 PI Donjon de Saint-Martin J, Montagnier L, Quillent C;
 XX
 DR WPI; 1996-230610/23.
 XX
 PT New antigenic HIV-1 group O strain proteins and related nucleic
 PT acids - useful in diagnosis, vaccines, therapy etc., of infection by
 PT HIV-1 group O strains VAU or DUR
 XX
 PS Claim 12; Page 58; 108pp; French.
 XX
 CC The invention relates to the isolation of a novel subgroup of the human
 CC immunodeficiency virus (HIV) type 1, designated group O. In particular,
 CC the inventors have isolated 2 new strains of the group O virus: strains
 CC VAU and DUR. Strain VAU was isolated from a French AIDS patient and has
 CC homology to the recently characterised Cameroonian HIV strains ANT70 and
 CC MPV5180. The DUR strain was isolated from a seropositive patient from
 CC the Cameroons who showed atypical seroreactivity. The peptides
 CC AAW07225-30 represent peptides derived from the strain DUR gp120 protein
 CC V3 loop. The DNA and protein sequences are used to generate peptides for
 CC detection of antibodies from patients infected with the new group O
 CC strains, as well as primers and probes to detect the viral nucleic acids.
 CC The peptides and nucleic acid sequences derived from these strains are
 CC able to distinguish between the group O and group M viral strains.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 15; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 5 KGA 7
 III
 RESULT 41
 AAW45343
 ID AAW45343 standard; peptide; 8 AA.
 XX
 AC AAW45343;
 XX
 DT 08-MAY-1998 (first entry)
 XX
 DE Beta-amyloid fragment (residues 24-31).
 XX
 KW Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment;

neurotrophin receptor p75; p75NTR; cyclic.
 Synthetic.
 Homo sapiens.
 WO9737228-A1.
 09-OCT-1997.
 28-MAR-1997; 97WO-US04966.
 29-MAR-1996; 96US-0625765.
 (UYBO-) UNIV BOSTON.
 Gilchrest BA, Yaar M;
 WPI; 1997-512306/47.
 Evaluating risk of individual to develop Alzheimer's - uses cultured
 epidermal melanocyte(s), also useful for developing therapies for
 neuro-degenerative diseases
 Disclosure; Page 10; 42pp; English.
 The present sequence represents residues 24 to 31 of beta-amyloid. A
 cyclic peptide was synthesised by attaching two cysteine residues to the
 beginning and the end of the fragment. The invention relates to a new
 method for evaluating the risk of an individual to develop Alzheimer's
 disease using cultured neural crest-derived melanocytes. Also
 described are methods of therapy for Alzheimer's disease using peptides
 (AAW45343-6) that bind to the neurotrophin receptor p75 nerve growth
 factor receptor (NGFR) and competitively inhibit the binding of a beta-
 amyloid to the p75 NGFR. The methods can be used for diagnosing and
 treating Alzheimer's disease and other neurodegenerative diseases
 mediated by beta-amyloid protein, or by aberrant activation of the low
 affinity NGFR localised on neural cell surfaces, such as autoimmune
 encephalomyelitis, Huntington's disease, cortico-basal degeneration,
 progressive supra-nuclear palsy, Gerotman-Shausleser Scheinker syndrome,
 Neimann-Pick disease, and progressive supranuclear palsy. In the
 diagnostic tests, the human melanocytes, which are easily obtainable
 from skin biopsies, are good model cells for the study and diagnosis of
 Alzheimer's disease.
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 15; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 5 KGA 7
 III
 RESULT 42
 AAW57531
 ID AAW57531 standard; peptide; 8 AA.
 XX
 AC AAW57531;
 XX
 DT 11-AUG-1998 (first entry)
 XX
 DE Molecular mimetic of unique N. meningitidis epitope, Pep 31.
 DE
 KW Molecular mimetic; epitope; serotype B; MenB; capsular polysaccharide;
 KW immune disease; non-autoreactive antibody; vaccine; passive immunisation;
 KW Escherichia coli K1 disease; bacterial meningitis; sepsis;
 KW oligosaccharide protein conjugate vaccine.
 XX
 OS Synthetic.
 OS Neisseria meningitidis.

```

PR 19-JUN-1992; 92US-0901523.
XX (JOSL-) JOSLIN DIABETES CENT.
XX Eisenbarth GS, Pietropaolo M;
XX WPI; 1993-167624/20.
XX
XX Neuro-endocrine protein antigen PM-1 - useful for treating
PT auto:immune diseases e.g. type I diabetes
XX
XX Claim 20; Page 38; 56pp; English.
XX
XX Sequence analysis of the PM-1 protein revealed two regions of
CC similarity with bovine serum albumin (BSA). These regions of
CC similarity may contain epitopes shared by the PM-1 molecule and BSA.
CC It has been shown that many patients with Type I diabetes have elevated
CC levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a
CC target antigen for cow milk induced islet autoimmunity. Peptides
CC comprising amino acids residues shared by the PM-1 protein and BSA
CC may be useful in the form of a therapeutic composition to treat an
CC autoimmune disease, such as Type I diabetes in an individual.
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 15; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGA 3
Db 2 KGA 4
XX
RESULT 38
AAR37286
ID AAR37286 standard; Protein; 8 AA.
XX
AC AAR37286;
XX
DT 06-SEP-1993 (first entry)
XX
DE PM-1/BSA peptide.
XX
KW Neuroendocrine; antigen; diabetes mellitus; pancrease; insulinoma;
KW PM-1; bovine serum albumin; BSA; epitope.
XX
OS Synthetic.
XX
PN WO9309141-A.
XX
PD 13-MAY-1993.
XX
PF 29-OCT-1992; 92WO-US09428.
XX
PR 01-NOV-1991; 91US-0788118.
PR 19-JUN-1992; 92US-0901523.
XX
XX (JOSL-) JOSLIN DIABETES CENT.
XX
XX Eisenbarth GS, Pietropaolo M;
XX
XX WPI; 1993-167624/20.
XX
XX Neuro-endocrine protein antigen PM-1 - useful for treating
XX auto:immune diseases e.g. type I diabetes
XX
XX Claim 20; Page 38; 56pp; English.
XX
XX Sequence analysis of the PM-1 protein revealed two regions of
CC similarity with bovine serum albumin (BSA). These regions of
CC similarity may contain epitopes shared by the PM-1 molecule and BSA.
CC It has been shown that many patients with Type I diabetes have elevated
CC levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a
CC target antigen for cow milk induced islet autoimmunity. Peptides
CC comprising amino acids residues shared by the PM-1 protein and BSA
CC may be useful in the form of a therapeutic composition to treat an
CC autoimmune disease, such as Type I diabetes in an individual.
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 15; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGA 3
Db 2 KGA 4
XX
RESULT 38
AAR37286
ID AAR37286 standard; Protein; 8 AA.
XX
AC AAR37286;
XX
DT 06-SEP-1993 (first entry)
XX
DE PM-1/BSA peptide.
XX
KW Neuroendocrine; antigen; diabetes mellitus; pancrease; insulinoma;
KW PM-1; bovine serum albumin; BSA; epitope.
XX
OS Synthetic.
XX
PN WO9309141-A.
XX
PD 13-MAY-1993.
XX
PF 29-OCT-1992; 92WO-US09428.
XX
PR 01-NOV-1991; 91US-0788118.
PR 19-JUN-1992; 92US-0901523.
XX
XX (JOSL-) JOSLIN DIABETES CENT.
XX
XX Eisenbarth GS, Pietropaolo M;
XX
XX WPI; 1993-167624/20.
XX
XX Neuro-endocrine protein antigen PM-1 - useful for treating
XX auto:immune diseases e.g. type I diabetes
XX
XX Claim 20; Page 38; 56pp; English.
XX
XX Sequence analysis of the PM-1 protein revealed two regions of
CC similarity with bovine serum albumin (BSA). These regions of
CC similarity may contain epitopes shared by the PM-1 molecule and BSA.
CC It has been shown that many patients with Type I diabetes have elevated

```

```

CC levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a
CC target antigen for cow milk induced islet autoimmunity. Peptides
CC comprising amino acids residues shared by the PM-1 protein and BSA
CC may be useful in the form of a therapeutic composition to treat an
CC autoimmune disease, such as Type I diabetes in an individual.
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 15; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGA 3
Db 2 KGA 4
XX
RESULT 39
AAR37287
ID AAR37287 standard; Protein; 8 AA.
XX
AC AAR37287;
XX
DT 06-SEP-1993 (first entry)
XX
DE PM-1/BSA peptide.
XX
KW Neuroendocrine; antigen; diabetes mellitus; pancrease; insulinoma;
KW PM-1; bovine serum albumin; BSA; epitope.
XX
OS Synthetic.
XX
PN WO9309141-A.
XX
PD 13-MAY-1993.
XX
PF 29-OCT-1992; 92WO-US09428.
XX
PR 01-NOV-1991; 91US-0788118.
PR 19-JUN-1992; 92US-0901523.
XX
XX (JOSL-) JOSLIN DIABETES CENT.
XX
XX Eisenbarth GS, Pietropaolo M;
XX
XX WPI; 1993-167624/20.
XX
XX Neuro-endocrine protein antigen PM-1 - useful for treating
XX auto:immune diseases e.g. type I diabetes
XX
XX Claim 20; Page 38; 56pp; English.
XX
XX Sequence analysis of the PM-1 protein revealed two regions of
CC similarity with bovine serum albumin (BSA). These regions of
CC similarity may contain epitopes shared by the PM-1 molecule and BSA.
CC It has been shown that many patients with Type I diabetes have elevated
CC levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a
CC target antigen for cow milk induced islet autoimmunity. Peptides
CC comprising amino acids residues shared by the PM-1 protein and BSA
CC may be useful in the form of a therapeutic composition to treat an
CC autoimmune disease, such as Type I diabetes in an individual.
XX
XX Sequence 8 AA;
SQ
Query Match 100.0%; Score 15; DB 14; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGA 3
Db 2 KGA 4

```

QY 1 KGA 3
 DB 3 KGA 5

RESULT 35
 AAM47142
 ID AAM47142 standard; Peptide; 7 AA.
 AC AAM47142;
 XX
 XX
 XX 12-FEB-2002 (first entry)
 DT
 XX
 XX S chrysomallus actinomycin biosynthesis protein acma fragment #6.
 DE
 XX Modular enzyme system; cyclic gene synthesis; repetitive coding sequence;
 KW antibiotic; non-ribosomal peptide synthetase; NRPS; PKS;
 KW polyketide synthase; actinomycin biosynthesis.
 XX
 XX Streptomyces chrysomallus.
 OS Synthetic.
 XX
 XX WO200181564-A2.
 PN
 XX
 PD 01-NOV-2001.
 PF 25-APR-2001; 2001WO-DE01578.
 XX
 XX 26-APR-2000; 2000DE-1021267.
 XX
 XX (ACTI-) ACTINODRUG PHARM GMBH.
 PA
 XX Schauwecker F;
 PI
 XX WPI; 2002-049276/06.
 DR N-PSDB; ABA03322.
 XX
 XX Preparing DNA encoding modular protein for e.g. producing new enzymes
 PT for synthesis of polyketide antibiotics, comprises cyclic integration
 PT of fragments into a vector
 XX
 XX Example 1; Page 44; 83pp; German.
 PS
 XX The present invention relates to the preparation of DNA, in a circular
 CC vector, that encodes one or more segments of a modular polypeptide. DNA
 CC or DNA libraries produced this way are used to produce modular
 CC polypeptides, particularly enzymes, which can be used to act on
 CC substrates to produce compounds for therapeutic testing. Enzymes of
 CC particular interest are those involved in non-ribosomal peptide synthesis
 CC or polyketide synthesis, and compounds for testing are particularly
 CC macrolide antibiotics, including penicillins, vancomycins or
 CC erythromycins, but may also be modular receptors. The present sequence is
 CC a fragment of protein encoded by a Streptomyces chrysomallus actinomycin
 CC biosynthesis gene which was used in a plasmid in the exemplification of
 CC the invention.

QY 1 KGA 3
 DB 3 KGA 5

RESULT 36
 AAR37284
 ID AAR37284 standard; Protein; 8 AA.
 XX
 XX AAR37284;
 AC

XX 06-SEP-1993 (first entry)
 DT
 XX PM-1/BSA peptide.
 DE
 XX Neuroendocrine; antigen; diabetes mellitis; pancreas; insulinoma;
 KW PM-1; bovine serum albumin; BSA; epitope.
 XX
 XX Synthetic.
 OS
 XX WO9309141-A.
 PN
 XX 13-MAY-1993.
 PD
 XX
 XX 29-OCT-1992; 92WO-US09428.
 PF
 XX 01-NOV-1991; 91US-0788118.
 PR 19-JUN-1992; 92US-0901523.
 XX
 XX (JOSL-) JOSLIN DIABETES CENT.
 PA
 XX Eisenbarth GS, Pietropaolo M;
 PI WPI; 1993-167624/20.
 XX
 XX Neuro-endocrine protein antigen PM-1 - useful for treating
 PT auto-immune diseases e.g. type I diabetes
 XX
 XX Claim 20; Page 38; 56pp; English.
 PS
 XX Sequence analysis of the PM-1 protein revealed two regions of
 CC similarity with bovine serum albumin (BSA). These regions of
 CC similarity may contain epitopes shared by the PM-1 molecule and BSA.
 CC It has been shown that many patients with Type I diabetes have elevated
 CC levels of anti-IgG anti-BSA antibodies. Thus, BSA may represent a
 CC target antigen for cow milk induced islet autoimmunity. Peptides
 CC comprising amino acids residues shared by the PM-1 protein and BSA
 CC may be useful in the form of a therapeutic composition to treat an
 CC autoimmune disease, such as Type I diabetes in an individual.
 XX
 XX Sequence 8 AA;
 SQ

Query Match 100.0%; Score 15; DB 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 DB 2 KGA 4

RESULT 37
 AAR37285
 ID AAR37285 standard; Protein; 8 AA.
 XX
 XX AAR37285;
 AC
 XX
 XX 06-SEP-1993 (first entry)
 DT
 XX PM-1/BSA peptide.
 DE
 XX Neuroendocrine; antigen; diabetes mellitis; pancreas; insulinoma;
 KW PM-1; bovine serum albumin; BSA; epitope.
 XX
 XX Synthetic.
 OS
 XX WO9309141-A.
 PN
 XX 13-MAY-1993.
 PD
 XX 29-OCT-1992; 92WO-US09428.
 PF
 XX 01-NOV-1991; 91US-0788118.
 PR

PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PI Cappello J;
 XX WPI; 1998-387091/33.
 DR
 XX New recombinant protein polymers - containing naturally occurring
 PT repetitive units for crosslinking by enzymes, useful as medical
 PT adhesives and sealants, depots and matrices
 XX
 PS Example 9; Column 49; 70pp; English.
 XX
 CC This is an example of a lysine donor peptide that can be
 CC utilised in novel recombinant protein polymers of the invention.
 CC Such polymers (see AAW9710-28) typically comprise a repetitive
 CC amino acid backbone of repetitive units having a collagen, fibroin,
 CC elastin or keratin motif and at least 2 enzyme recognition
 CC sequences comprising a glutamine and/or lysine capable of enzyme
 CC catalysed isopeptide formation. The polymers are capable of
 CC covalent crosslinking by enzymatic reaction to form products which
 CC set quickly and have good adhesive properties and high strength.
 CC They can be used as medical adhesives and sealants, in the closure
 CC of wounds and repair of damaged tissues, prosthesis coatings, drug
 CC depots, and matrices for the transplantation of cells.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 15; DB 19; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB III
 5 KGA 7
 DE
 RESULT 33
 ID AAW93020 standard; peptide; 7 AA.
 AC AAW93020;
 XX 18-MAY-1999 (first entry)
 DT DE19725619 peptide #11.
 DE
 XX Agonist; cytotoxic; competitive inhibitor; amyloid formation; treatment;
 KW type II diabetes mellitus; Alzheimer's disease; CJD; scrapie; BSE;
 KW spongiform encephalopathy.
 XX Synthetic.
 OS
 XX DE19725619-A1.
 PN
 XX 24-DEC-1998.
 PD
 XX 17-JUN-1997; 97DE-1025619.
 PF
 XX 17-JUN-1997; 97DE-1025619.
 PR
 XX (FRAU) FRAUNHOFER GES FORDERUNG ANGEWANDTEN.
 PA
 XX Bernhagen J, Brunner H, Kapurniotu A;
 PI
 XX WPI; 1999-121938/11.
 DR
 XX Peptides containing amino acid sequence GA - useful for inhibiting
 PT amyloid formation and associated cytotoxicity in the treatment of
 PT type II diabetes mellitus
 XX
 XX Claim 5; Column 5; 8pp; German.
 PS
 XX This invention describes novel agonists (competitive inhibitor) and/or

CC inhibitors of amyloid formation peptides which are 3-15 amino acids in
 CC length and contain at least the active sequence GA. The new peptides
 CC are useful for inhibiting amyloid formation and associated cytotoxicity
 CC in the treatment of type II diabetes mellitus, Alzheimer's disease and
 CC spongiform encephalopathies (e.g. CJD, scrapie and BSE).
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 15; DB 20; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB III
 3 KGA 5
 DE
 RESULT 34
 ID AAW47140 standard; Peptide; 7 AA.
 XX AAW47140;
 AC
 XX 12-FEB-2002 (first entry)
 DT
 XX S chrysomallus actinomycin biosynthesis protein acmA fragment #4.
 DE
 KW Modular enzyme system; cyclic gene synthesis; repetitive coding sequence;
 KW antibiotic; non-ribosomal peptide synthetase; NRPS; PKS;
 KW polyketide synthase; actinomycin biosynthase.
 XX
 XX Streptomyces chrysomallus.
 OS
 XX Synthetic.
 XX WO200181564-A2.
 PN
 XX 01-NOV-2001.
 PD
 XX 25-APR-2001; 2001WO-DE01578.
 PF
 XX 26-APR-2000; 2000DE-1021267.
 PR
 XX (ACTI-) ACTINODRUG PHARM GMBH.
 PA
 PI Schawecker F;
 XX
 XX WPI; 2002-049276/06.
 DR
 DR N-PSDB; ABA03318.
 XX
 PT Preparing DNA encoding modular protein for e.g. producing new enzymes
 PT for synthesis of polyketide antibiotics, comprises cyclic integration
 PT of fragments into a vector -
 XX
 XX Example 1; Page 43; 83pp; German.
 PS
 XX The present invention relates to the preparation of DNA, in a circular
 CC vector, that encodes one or more segments of a modular polypeptide. DNA
 CC or DNA libraries produced this way are used to produce modular
 CC polypeptides, particularly enzymes, which can be used to act on
 CC substrates to produce compounds for therapeutic testing. Enzymes of
 CC particular interest are those involved in non-ribosomal peptide synthesis
 CC or polyketide synthesis, and compounds for testing are particularly
 CC macrolide antibiotics, including penicillins, vancomycins or
 CC erythromycins, but may also be modular receptors. The present sequence is
 CC a fragment of protein encoded by a Streptomyces chrysomallus actinomycin
 CC biosynthesis gene which was used in a plasmid in the exemplification of
 CC the invention.
 XX
 XX Sequence 7 AA;
 SQ
 Query Match 100.0%; Score 15; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

AC AAR80377;
XX
XX
DT 19-APR-1996 (first entry)
XX
DE Protein polymeric adhesion substrate lysine donor peptide #7.
XX
XX
KW Pendant group; repeating unit; enzyme recognition site; sealant; fibrin;
KW enzymatic cross-linking; biocompatible material; structural integrity;
KW medical adhesive; wound closure; tissue repair; transglutaminase;
KW protein polymer adhesive substrate.
XX
XX Synthetic.
XX
XX W09523611-A1.
XX
XX
XX PD 08-SEP-1995.
XX
XX PF 03-MAR-1995; 95WO-US02728.
XX
XX PR 03-MAR-1994; 94US-0205518.
XX
XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX
XX PI Cappello J;
XX
XX DR WPI; 1995-320413/41.
XX
XX
XX PT Protein polymers comprising repeating units and sequences - capable
XX of enzyme-catalysed covalent bond formation useful as a
XX biocompatible material for wound closure and tissue repair
XX
XX Example 9; Page 75; 138pp; English.
XX
XX The peptides AAR80371-7 are examples of lysine donor peptides which
XX can be used to generate protein polymeric adhesion substrate (PPAS)
XX contg. repeats of non-fibrin cross-linking donor peptide sequences (see
XX AAR80345-50 for examples of PPAS proteins). The PPAS proteins can be
XX used as substrates in enzymatic cross-linking reactions catalysed by a
XX transglutaminase enzyme e.g. Factor VIII or XIII. The polymers can be
XX used in biological systems where in situ formation of a biocompatible
XX material with structural integrity is required e.g. as medical adhesives
XX and sealants or for wound closure or tissue repair.
XX
XX SQ Sequence 7 AA;
Query Match 100.0%; Score 15; DB 16; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
DB 5 KGA 7

RESULT 31
AAW72631
ID AAW72631 standard; peptide; 7 AA.
XX
XX AC AAW72631;
XX
XX DT 06-JAN-1999 (first entry)
XX
XX DE Conus genus omega-conopeptide group 1 fragment.
XX
XX KW Conus genus; marine snail; cone snail; omega-conopeptide; analgesia;
KW nociceptive pain; neuropathic pain; neuronal tissue; conotoxin;
KW inflammation; schizophrenia; tardive dyskinesia; acute dystonic reaction;
KW rheumatoid arthritis; epilepsy.
XX
XX OS Conus sp.
XX
XX FH Key Location/Qualifiers
XX Misc-difference 7

/label= Lys, Ser
US5824645-A.
20-OCT-1998.
01-NOV-1996; 96US-0742774.
15-APR-1993; 93US-0049794.
30-DEC-1991; 91US-0814759.
03-JUL-1996; 96US-0675354.
01-NOV-1996; 96US-0742774.
(NEUR-) NEUREX CORP.
Gohil KC, Justice A, Miljanich GP, Singh T, Valentino KL;
WPI; 1998-582596/49.
Treatment of inflammation, comprises administration of
omega-conopeptide - effective to block voltage-gated calcium
channels, bind with high affinity to omega-conopeptide binding site,
and inhibit neuro-transmitter release
Disclosure; Column 55; 58pp; English.
A method has been developed for the treatment of inflammation in a
subject. The method comprises administration of an omega-conopeptide
effective to: (i) block voltage-gated calcium channels; (ii) bind with
high affinity to an omega-conopeptide binding site; and (iii) inhibit
neurotransmitter release from nervous tissue. The method is used to
treat inflammation and associated pain. The treatment can also be used
to produce analgesia (especially in subjects experiencing neuropathic
pain); and to treat schizophrenia, tardive dyskinesia and acute dystonic
reactions, rheumatoid arthritis, and epilepsy. The present sequence
represents a omega-conopeptide group 1 fragment. Omega-conopeptides are
components of peptide toxins produced by marine snails of the genus
Conus, and which act as calcium channel blockers.
Sequence 7 AA;
Query Match 100.0%; Score 15; DB 19; Length 7;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
DB 4 KGA 6

RESULT 32
AAW49762
ID AAW49762 standard; Peptide; 7 AA.
XX
XX AC AAW49762;
XX
XX DT 12-OCT-1998 (first entry)
XX
XX DE Lysine donor peptide.
XX
XX KW Protein polymer; adhesive sealant; wound healing; cross-linking.
XX
XX OS Synthetic.
XX
XX PN US5773577-A.
XX
XX PD 30-JUN-1998.
XX
XX PF 03-MAR-1994; 94US-0205518.
XX
XX PR 02-MAR-1995; 95US-0397633.
XX 03-MAR-1994; 94US-0205518.
XX

```

XX Sequence 6 AA; Query Match 100.0%; Score 15; DB 21; Length 6;
 SQ Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 DB 4 KGA 6

RESULT 28
 AAB19468
 ID AAB19468 standard; peptide; 6 AA.
 XX AC AAB19468;
 XX DT 06-MAR-2001 (first entry)
 XX DE Amino acid sequence of a fragment of an omega-conopeptide.
 XX OS Omega-conopeptide; voltage-gated calcium channel inhibitor; analgesic;
 KW peptide toxin; opiate; pain; neuronal damage; ischemic condition;
 KW schizophrenia; tardive dyskinesia; acute dystonic reaction; inflammation;
 KW epilepsy.
 XX OS Conus sp.
 XX PN US6136786-A.
 XX PD 24-OCT-2000.
 XX PF 09-SEP-1999; 99US-0392979.
 XX PR 01-NOV-1996; 96US-0742774.
 PR 30-DEC-1991; 91US-0814759.
 PR 15-APR-1993; 93US-0049794.
 PR 03-JUL-1996; 96US-0675354.
 PR 21-AUG-1998; 98US-0138439.
 PR 23-APR-1999; 99US-0296017.
 PR 23-JUN-1993; 93US-0081863.
 XX PA (ELAN-) ELAN PHARM INC.
 XX PI Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;
 XX WPI; 2001-030946/04.
 XX Enhancing analgesia produced by opiates by administering an
 PT omega-conopeptide that inhibits electrically stimulated contraction of
 PT guinea pig ileum and binds to omega-conopeptide MVIIA binding sites in
 PT neuronal tissues -
 XX Disclosure; Column 53-54; 58pp; English.
 XX AAB19468-72 represent fragments of omega-conopeptides.
 CC Omega-conopeptides are components of peptide toxins which act as
 CC voltage-gated calcium channel inhibitors. The peptides are used to
 CC enhance the analgesic effect produced by an opiate in a mammalian
 CC subject. The method comprises administering to the subject an
 CC omega-conopeptide which is able to inhibit electrically stimulated
 CC contraction of the guinea pig ileum and bind to omega-conopeptide MVIIA
 CC binding sites present in neuronal tissue. Omega-conopeptides are useful
 CC for enhancing the analgesic effect produced by an opiate.
 CC Omega-conopeptides may also be used in the treatment of pain, in reducing
 CC neuronal damage related to an ischemic condition in mammals, and in
 CC treating schizophrenia, tardive dyskinesia and acute dystonic reactions,
 CC inflammation and epilepsy.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 15; DB 22; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 DB 4 KGA 6

RESULT 29
 AAM47138
 ID AAM47138 standard; Peptide; 6 AA.
 XX AC AAM47138;
 XX DT 12-FEB-2002 (first entry)
 XX DE S chrysomallus actinomycin biosynthesis protein acmA fragment #2.
 XX KW Modular enzyme system; cyclic gene synthesis; repetitive coding sequence;
 KW antibiotic; non-ribosomal peptide synthetase; NRPS; PKS;
 KW polyketide synthase; actinomycin biosynthesis.
 XX OS Streptomyces chrysomallus.
 XX PN WO200181564-A2.
 XX PD 01-NOV-2001.
 XX PF 25-APR-2001; 2001WO-DE01578.
 XX PR 26-APR-2000; 2000DE-1021267.
 XX PA (ACTI-) ACTINODRUG PHARM GMBH.
 XX PI Schauwecker F;
 XX WPI; 2002-049276/06.
 XX N-PSDB; ABA03316.
 XX Preparing DNA encoding modular protein for e.g. producing new enzymes
 PT for synthesis of polyketide antibiotics, comprises cyclic integration
 PT of fragments into a vector -
 XX Example 1; Page 43; 83pp; German.
 XX The present invention relates to the preparation of DNA, in a circular
 CC vector, that encodes one or more segments of a modular polypeptide. DNA
 CC or DNA libraries produced this way are used to produce modular
 CC polypeptides, particularly enzymes, which can be used to act on
 CC substrates to produce compounds for therapeutic testing. Enzymes of
 CC particular interest are those involved in non-ribosomal peptide synthesis
 CC or polyketide synthesis, and compounds for testing are particularly
 CC macrolide antibiotics, including penicillins, vancomycins or
 CC erythromycins, but may also be modular receptors. The present sequence is
 CC a fragment of a protein encoded by a Streptomyces chrysomallus
 CC actinomycin biosynthesis gene which was used in the exemplification of
 CC the invention.
 XX Sequence 6 AA;
 SQ Query Match 100.0%; Score 15; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 DB 3 KGA 5

RESULT 30
 AAR80377
 ID AAR80377 standard; peptide; 7 AA.
 XX

XX New pyrrolobenzodiazepine derivatives used in the preparation of
PT combinatorial libraries of further pyrrolobenzodiazepine derivatives
PT
XX
PS Example 8; Page 72; 158pp; English.
XX The invention relates to novel pyrrolobenzodiazepine (PBD) derivatives
CC which are compounds that bind to the minor groove of double stranded
CC nucleic acid sequences, especially at the sequence Purine-Guanine-Purine
CC where Purine is selected from adenine and guanine. The PBD's can be used
CC in combinatorial peptide library screening for binding interactions with
CC nucleic acids. The PBD's can be used in cytotoxic, antibiotic,
CC antiparasitic and antiviral compositions and also in methods of
CC diagnosis and in methods of target validation in functional genomics. The
CC peptides AAY83826-Y83833 represent PBD-peptides isolated from a
CC combinatorial peptide library screen on the target nucleic acid sequence
CC AAZ99178.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 15; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGA 3
DB 3 KGA 5

RESULT 26
AAY83831
ID AAY83831 standard; peptide; 6 AA.
XX
XX AAY83831;
XX
XX 05-JUL-2000 (first entry)
DT
DE Pyrrolobenzodiazepine-peptide #6 from combinatorial library screen.
XX
XX Antibacterial; antiparasitic; cytostatic; pyrrolobenzodiazepine;
KW DNA minor groove; combinatorial peptide library screening; virucide;
KW cytotoxic.
XX
XX Synthetic.
OS
XX Key Location/Qualifiers
FH Modified-site 1
FT /note= "conjugated to pyrrolobenzodiazepine group"
FT
XX
XX W0200012506-A2.
PN
XX
XX 09-MAR-2000.
PD
XX
XX 27-AUG-1999; 99WO-GB02836.
PF
XX
XX 27-AUG-1998; 98GB-0018730.
PR
XX
XX (UYPO-) UNIV FORTSMOUTH HIGHER EDUCATION CORP.
PA
XX
XX Thurston DE, Howard PW;
PI
XX
XX WPI; 2000-237841/20.
DR
XX
XX New pyrrolobenzodiazepine derivatives used in the preparation of
PT combinatorial libraries of further pyrrolobenzodiazepine derivatives
PT
XX
XX Example 8; Page 72; 158pp; English.
PS The invention relates to novel pyrrolobenzodiazepine (PBD) derivatives
CC which are compounds that bind to the minor groove of double stranded
CC nucleic acid sequences, especially at the sequence Purine-Guanine-Purine

CC where Purine is selected from adenine and guanine. The PBD's can be used
CC in combinatorial peptide library screening for binding interactions with
CC nucleic acids. The PBD's can be used in cytotoxic, antibiotic,
CC antiparasitic and antiviral compositions and also in methods of
CC diagnosis and in methods of target validation in functional genomics. The
CC peptides AAY83826-Y83833 represent PBD-peptides isolated from a
CC combinatorial peptide library screen on the target nucleic acid sequence
CC AAZ99178.
XX
SQ Sequence 6 AA;
Query Match 100.0%; Score 15; DB 21; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KGA 3
DB 1 KGA 3

RESULT 27
AAY56506
ID AAY56506 standard; peptide; 6 AA.
XX
XX AAY56506;
XX
XX 16-FEB-2000 (first entry)
DT
DE Peptide SEQ ID NO:22.
XX
XX Omega conopeptide; analgesic; nociceptive; neuropathic; pain;
KW conotoxin; marine snail; peptide toxin; inflammation; binding;
KW voltage-gated calcium channel; inhibition; norepinephrine;
KW noradrenaline; anti-inflammatory.
XX
XX Synthetic.
OS
XX US5994305-A.
PN
XX 30-NOV-1999.
PD
XX
XX 21-AUG-1998; 98US-0138439.
PF
XX
XX 01-NOV-1996; 96US-0742774.
PR
XX 15-APR-1993; 93US-0049794.
PR
XX 03-JUL-1996; 96US-0675354.
PR
XX 30-DEC-1991; 91US-0814759.
XX
XX (ELAN-) ELAN PHARM INC.
PA
XX
XX Justice A, Singh T, Valentino KL, Miljanich GP, Gohil KC;
PI
XX WPI; 2000-038270/03.
DR
XX
XX Measuring the activity of test compounds in blocking voltage-gated
PT calcium channels, binding to the omega conopeptide binding site and
PT inhibiting norepinephrine (noradrenaline) release for treating
PT inflammation -
XX
XX Disclosure; Column 17; 47pp; English.

XX A method has been developed of selecting a test compound for treating
CC inflammation. The method comprises measuring the activity of the test
CC compound in blocking voltage-gated calcium channels, binding to the
CC omega conopeptide binding site and inhibiting norepinephrine
CC (noradrenaline) release from nervous tissue. The method is useful for
CC selecting compounds for treating inflammation. The selected compounds
CC are capable of producing analgesia in a mammalian subject with chronic
CC or intractable pain. Analgesia caused by selected compounds may cause
CC the reliance on opioid analgesic agents of the prior art which cause
CC dependency and tolerance, requiring potentially dangerous increases in
CC opioid doses to achieve the analgesic effect. The present sequence
CC represents a peptide given in the present invention.

QY 1 KGA 3
 DB 4 KGA 6

RESULT 21

AA95764
 ID AA95764 standard; Peptide; 6 AA.

AC AA95764;

XX 07-NOV-2000 (first entry)

XX Inhibiting enterocyte growth factor IEGF15.

XX IEGF15; inhibiting enterocyte growth factor; enterocytogenin;
 KW nucleopeptide; proliferative; antiproliferative; antitumour;
 KW morphogenesis; cancer; therapy.

XX Mammalia.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal adenosine"
 FT Modified-site 6 /note= "C-terminal amide"

XX WO200047605-A2.

XX 17-AUG-2000.

XX 07-FEB-2000; 2000WO-BG000005.

XX 12-FEB-1999; 99BG-0103173.

XX (TCHO/) TCHOBANOVA A A.

XX Alexandrov CA, Trifonov BB, Roussev GK;

XX WPI; 2000-565282/52.

XX Novel enterocyte growth factors and method for their isolation from
 PT intestinal mucosa, useful for treating e.g. cancer -

XX Claim 15; Page 38; 48pp; English.

XX The present sequence is that of inhibiting enterocyte growth
 CC factor IEGF15 (mol.wt. 1.20-1.40 kDa). The invention provides
 CC stimulating and inhibiting enterocyte growth factors
 CC (enterocytogenins) (see AA95755-69) that influence the speed of
 CC morphogenesis, either stimulating or inhibiting cell growth. The
 CC enterocyte growth factors are nucleopeptides that can be isolated
 CC from the intestinal mucosa of warm-blooded animals, such as pigs,
 CC rats, dogs etc., using a claimed method of the invention. They
 CC are useful for modulating morphogenesis, e.g. in the treatment of
 CC cancers, and have higher effectiveness than previous stimulators
 CC and inhibitors of cell division.

XX Sequence 6 AA;

Query Match 100.0%; Score 15; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 DB 2 KGA 4

RESULT 22

AA95765
 ID AA95765 standard; Peptide; 6 AA.

XX AC

XX AA95765;

XX 07-NOV-2000 (first entry)

XX Inhibiting enterocyte growth factor IEGF16.

XX IEGF16; inhibiting enterocyte growth factor; enterocytogenin;
 KW nucleopeptide; proliferative; antiproliferative; antitumour;
 KW morphogenesis; cancer; therapy.

XX Mammalia.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "N-terminal guanosine"
 FT Modified-site 6 /note= "C-terminal amide"

XX WO200047605-A2.

XX 17-AUG-2000.

XX 07-FEB-2000; 2000WO-BG000005.

XX 12-FEB-1999; 99BG-0103173.

XX (TCHO/) TCHOBANOVA A A.

XX Alexandrov CA, Trifonov BB, Roussev GK;

XX WPI; 2000-565282/52.

XX Novel enterocyte growth factors and method for their isolation from
 PT intestinal mucosa, useful for treating e.g. cancer -

XX Claim 16; Page 38; 48pp; English.

XX The present sequence is that of inhibiting enterocyte growth
 CC factor IEGF16 (mol.wt. 1.10-1.30 kDa). The invention provides
 CC stimulating and inhibiting enterocyte growth factors
 CC (enterocytogenins) (see AA95755-69) that influence the speed of
 CC morphogenesis, either stimulating or inhibiting cell growth. The
 CC enterocyte growth factors are nucleopeptides that can be isolated
 CC from the intestinal mucosa of warm-blooded animals, such as pigs,
 CC rats, dogs etc., using a claimed method of the invention. They
 CC are useful for modulating morphogenesis, e.g. in the treatment of
 CC cancers, and have higher effectiveness than previous stimulators
 CC and inhibitors of cell division.

XX Sequence 6 AA;

Query Match 100.0%; Score 15; DB 21; Length 6;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 DB 2 KGA 4

RESULT 23

AA95766
 ID AA95766 standard; Peptide; 6 AA.

XX AA95766;

XX 07-NOV-2000 (first entry)

XX Inhibiting enterocyte growth factor IEGF17.

XX IEGF17; inhibiting enterocyte growth factor; enterocytogenin;
 KW nucleopeptide; proliferative; antiproliferative; antitumour;

XX Disclosure; Column 17; 59pp; English.

PS Sequences AAW95590-594 represent fragments within omega-conopeptides

CC group 1 and 2. Omega-conopeptides are components of peptide toxins

CC produced by marine snails of the genus Conus, and which act as calcium

CC channel blockers. The invention relates to a method of producing

CC analgesia in a mammal that comprises administering an omega-conopeptide

CC having activities in (a) inhibiting electrically stimulated contraction

CC of guinea pig ileum and (b) selectively binding to omega-conopeptide

CC MWIIA binding sites in neuronal tissue, where these activities are

CC within the ranges of those of omega-conotoxins MWIIA and TVIA. The

CC method is used for treating chronic pain, especially neuropathic pain.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 15; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3

DB 4 KGA 6

RESULT 19

AAW90100

ID AAW90100 standard; Protein; 6 AA.

AC AAW90100;

XX

XX 15-MAR-1999 (first entry)

XX

DE Rat CART (62-102) protease digestion fragment #2.

XX

KW CART; cocaine and amphetamine regulated transcript; rat; anorectic;

KW appetite regulator; treatment; obesity; type II diabetes; bulimia;

KW autoimmune disease; inflammation; arthritis; type I diabetes; menopause;

KW multiple sclerosis; stroke; osteoporosis; Parkinson's disease; adipsia;

XX menstrual complication; cancer.

OS Rattus sp.

XX

XX WO9842747-A1.

XX

PD 01-OCT-1998.

XX

PF 26-MAR-1998; 98WO-DK00128.

XX

XX 19-NOV-1997; 97DK-0001315.

PR 26-MAR-1997; 97DK-0000358.

XX

PA (NOVO) NOVO-NORDISK AS.

XX

XX Christiansen K, Hastrup S, Judge ME, Kristensen P;

PI Tim L;

PI

XX WPI; 1999-045136/04.

XX

XX New isolated cocaine and amphetamine regulated transcript proteins -

PT with anorectic and adipsic activity, useful for regulating appetite,

PT particularly for treating obesity, also related nucleic acid,

PT vectors, transgenic organisms and antibodies

XX

PS Example 8; Page 37; 80pp; English.

XX

XX This sequence represents a rat cocaine and amphetamine regulated

CC transcript (CART) protein fragment which has been subjected to a

CC protease digestion using an Amillaria mellea protease. The CART protein

CC and its fragments have anorectic activity and are used to regulate

CC appetite and in the treatment of obesity as well as type II diabetes and

CC bulimia). They may also be useful in treating autoimmune disease,

CC inflammation, arthritis, type I diabetes, multiple sclerosis, stroke,

CC

CC osteoporosis, menopausal symptoms, menstrual complications and

CC Parkinson's disease. CART is the protein responsible for the anorectic

CC and adipsic phenotype associated with certain cancers.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 15; DB 20; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3

DB 1 KGA 3

RESULT 20

AAAB14373

ID AAB14373 standard; peptide; 6 AA.

XX

XX AAB14373;

AC

XX 06-DEC-2000 (first entry)

XX

DE Conopeptide group 1 fragment #1.

XX

KW Marine snail; omega-conopeptide; calcium channel blocker;

KW toxin; analgesic; antiinflammatory; anticonvulsant; neuroleptic;

KW norepinephrine release inhibitor; schizophrenia; tardive dyskinesia;

KW acute dystonic reaction; inflammation; epilepsy.

XX

OS Conus sp.

XX

XX US6087091-A.

XX

PD 11-JUL-2000.

XX

XX 23-APR-1999; 99US-0298017.

XX

PR 01-NOV-1996; 96US-0742774.

PR 15-APR-1993; 93US-0049794.

PR 03-JUL-1996; 96US-0675354.

PR 21-AUG-1998; 98US-0138439.

PR 30-DEC-1991; 91US-0814759.

XX

PA (ELAN-) ELAN PHARM INC.

XX

XX Singh T, Gohil KC, Valentino KL, Miljanich GP, Justice A;

PI WPI; 2000-490177/43.

XX

XX Selecting a compound for producing analgesia involves measuring

PT activity of test compound in blocking voltage-gated calcium channels,

PT binding to omega conopeptide binding site and inhibiting norepinephrine

PT release

XX

XX Disclosure; Column 53-54; 58pp; English.

PS

XX

XX The present sequence is a fragment of an omega-conopeptide.

CC Omega-conopeptides are components of peptide toxins produced marine

CC snails of the genus Conus. Omega-conopeptides and their derivatives act

CC as calcium channel blockers and may be useful for producing analgesia in

CC nociceptive and neuropathic pain. The peptides bind to omega-conopeptide

CC binding sites, which are present mainly in neuronal tissue, and inhibit

CC norepinephrine release from nervous tissue. Conopeptides such as MWIIA

CC and TVIA are effective as therapeutic agents for treating neurogenic

CC conditions such as schizophrenia, tardive dyskinesia and acute dystonic

CC reactions, inflammation and epilepsy.

XX

SQ Sequence 6 AA;

Query Match 100.0%; Score 15; DB 21; Length 6;

Best Local Similarity 100.0%; Pred. No. 7.8e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OS Synthetic.
 XX FH Key
 XX FT Modified-site 1 Location/Qualifiers
 XX FT /note= "N-terminus is attached via a peptide bond to
 the C-terminus amino acid at position 6"
 XX FT Modified-site 6
 XX FT /note= "C-terminus is attached via a peptide bond to
 the N-terminus amino acid at position 1"
 XX FT
 XX PN W09939728-A2.
 XX PD 12-AUG-1999.
 XX PF 03-FEB-1999; 99WO-US02362.
 XX PR 04-FEB-1998; 98US-0018194.
 XX PA (UYBO-) UNIV BOSTON.
 XX PI Eller M, Gilchrest BA, Yaar M;
 XX DR WPI; 1999-539950/45.
 XX CC Controlling or manipulating melanocyte and keratinocyte cell death,
 useful for treating, e.g. alopecia areata
 XX PS Claim 4; Page 40; 67pp; English.
 XX CC This sequence is a cyclic peptide which competes with and competitively
 inhibits beta-amyloid binding to the p75 neurotrophin receptor (p75NTR).
 CC p75NTR is a low affinity nerve growth factor (NGF) receptor which is
 expressed by melanocytes and keratinocytes of the basal epidermis.
 CC Apoptosis can be inhibited by p75NTR via the upregulation of the Bcl-2
 protein. If the receptor is occupied by appropriate ligands e.g.
 CC neurotrophins, apoptosis is inhibited. Other examples of appropriate
 CC ligands include this cyclic peptide. This peptide is based on the
 CC sequence of the binding fragment of beta-amyloid, which binds to
 CC p75NTR in Alzheimer's disease. This cyclic peptide can be used in
 CC methods to control or manipulate keratinocyte or melanocyte cell death.
 CC The methods involve using this peptide or peptides AAY39233-V39234 to
 CC bind as a pseudo-ligand to the p75 neurotrophin receptor, inhibiting
 CC apoptosis. The new method can induce or maintain hair growth, hair colour
 CC or skin colour. Inducing or maintaining hair growth is useful for
 CC treating alopecia areata or male pattern baldness in vertebrates.
 XX SQ Sequence 6 AA;
 XX Query Match 100.0%; Score 15; DB 20; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 KGA 3
 XX |||
 XX DB 2 KGA 4
 XX
 XX RESULT 17
 XX AAW93019
 XX ID AAW93019 standard; peptide; 6 AA.
 XX AC AAW93019;
 XX XX
 XX DT 18-MAY-1999 (first entry)
 XX DE DE19725619 peptide #10.
 XX XX Agonist; cytotoxic; competitive inhibitor; amyloid formation; treatment;
 XX KW type II diabetes mellitus; Alzheimer's disease; CJD; scrapie; BSE;
 XX KW spongiform encephalopathy.
 XX OS Synthetic.
 XX Q5

XX PN DE19725619-A1.
 XX XX
 XX PD 24-DEC-1998.
 XX XX
 XX PF 17-JUN-1997; 97DE-1025619.
 XX XX
 XX PR 17-JUN-1997; 97DE-1025619.
 XX XX
 XX PA (FRAU) FRAUNHOFER GES FOERDERUNG ANGEWANDTEN.
 XX XX
 XX PI Bernhagen J, Brunner H, Kapurniotu A;
 XX DR WPI; 1999-121938/11.
 XX XX
 XX PT Peptides containing amino acid sequence GA - useful for inhibiting
 amyloid formation and associated cytotoxicity in the treatment of
 PT type II diabetes mellitus
 XX PS Claim 5; Column 5; 8pp; German.
 XX CC This invention describes novel agonists (competitive inhibitor) and/or
 CC inhibitors of amyloid formation peptides which are 3-15 amino acids in
 CC length and contain at least the active sequence GA. The new peptides
 CC are useful for inhibiting amyloid formation and associated cytotoxicity
 CC in the treatment of type II diabetes mellitus, Alzheimer's disease and
 CC spongiform encephalopathies (e.g. CJD, scrapie and BSE).
 XX SQ Sequence 6 AA;
 XX Query Match 100.0%; Score 15; DB 20; Length 6;
 XX Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 XX Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX QY 1 KGA 3
 XX |||
 XX DB 2 KGA 4
 XX
 XX RESULT 18
 XX AAW95590
 XX ID AAW95590 standard; protein; 6 AA.
 XX AC AAW95590;
 XX XX
 XX DT 29-MAR-1999 (first entry)
 XX DE DE
 XX DE Conopeptide group 1 fragment.
 XX KW Omega-conopeptide; peptide toxin; snail; calcium channel blocker;
 KW analgesia; guinea pig ileum; omega-conotoxin; pain; neuropathic.
 XX OS Synthetic.
 XX OS Conus sp.
 XX PN US5859186-A.
 XX XX
 XX PD 12-JAN-1999.
 XX XX
 XX PF 03-JUL-1996; 96US-0675354.
 XX XX
 XX PR 15-APR-1993; 93US-0049794.
 XX PR 30-DEC-1991; 91US-0814759.
 XX PR 03-JUL-1996; 96US-0675354.
 XX XX
 XX PA (NEUR-) NEUREX CORP.
 XX XX
 XX PI Gohlil KC, Justice A, Miljanich GP, Singh T, Valentino KL;
 XX DR WPI; 1999-120002/10.
 XX XX
 XX PT Production of analgesia in mammal - by administration of omega
 PT cono-peptide(s)

```

PT endothelin function
XX PS Claim 1; Page 1; 8pp; Japanese.
XX
CC A novel peptide comprising at least four residues from the
CC contiguous amino acid sequence shown, is capable of binding
CC endothelin or its precursor. The peptide is useful for determining
CC the presence of endothelin and as an agent for preventing or
CC inhibiting the action of endothelin.
XX See also AAR34870-80.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 15; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
   |||
Db 1 KGA 3

RESULT 14
AAR39597
ID AAR39597 standard; peptide; 6 AA.
XX
AC AAR39597;
XX
XX 08-DEC-1993 (first entry)
XX
XX Leukocyte Response Integrin ligand peptide.
XX
XX LRI; beta-integrin; cytoadhesin; ligand-binding specificity;
XX polymorphonuclear neutrophil; integrin-associated protein; IAP.
XX
XX Synthetic.
XX
XX US225531-A.
XX
XX 06-JUL-1993.
XX
XX 09-APR-1992; 92US-0866678.
XX
XX 09-APR-1992; 92US-0866678.
XX
XX (UNIW ) UNIV WASHINGTON.
XX
XX Adams SP, Brown EJ, Gresham HD;
XX
XX WPI; 1993-226662/28.
XX
XX Peptide of lysine glycine alanine glycine aspartic acid valine
XX amino acid chain - comprises ligand for leukocyte response
XX integrin, inhibiting fibrinogen-dependent activation of
XX polymorphonuclear neutrophil
XX
XX Claim 1; Column 20; 19pp; English.
XX
CC A hexapeptide sequence present in the gamma chain of native fibrinogen
CC (see AAR39599) was mutated by the single substitution of a glycine for a
CC glutamine to produce KGAGDV (AAR39597). The novel peptide was found
CC to retain Leukocyte Response Integrin ligand binding and PMN
CC activation. Antibodies to the beta1 and beta2 integrin families had
CC no effect on KGAGDV binding to LRI; antibodies to both beta3 and
CC Integrin-Associated Protein inhibited KGAGDV binding to LRI.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 15; DB 14; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
   |||
Db 1 KGA 3

endothelin function
|||
1 KGA 3

Db 1 KGA 3

RESULT 15
AAR8666
ID AAR8666 standard; Protein; 6 AA.
XX
AC AAR8666;
XX
XX 30-AUG-1996 (first entry)
XX
XX N.meningitidis IM2394 transferrin receptor Tbp2 domain 1 epitope.
XX
XX Transferrin receptor; Tbp2 subunit; deletion mutant; vaccine;
XX passive immunisation; immunotherapy; monoclonal antibody.
XX
XX Neisseria meningitidis (strain IM2394).
XX
XX WO9533049-A2.
XX
XX 07-DEC-1995.
XX
XX 30-MAY-1995; 95WO-FR00701.
XX
XX 31-MAY-1994; 94FR-0006594.
XX
XX (INMR ) PASTEUR MERIEUX SERUMS & VACCINS.
XX (TRGE ) TRANSGENE SA.
XX
XX Jacobs E, Legrain M, Mazarin V, Lissolo L;
XX Millet MBJ;
XX
XX WPI; 1996-030562/03.
XX
XX Polypeptide(s) for vaccination against Neisseria meningitidis group
XX B - comprising deletion mutants of transferrin receptor Tbp2
XX subunit
XX
XX Claim 50; Page 96; 114pp; French.
XX
XX Claimed monoclonal antibodies recognise an epitope in the first
XX domain of a N.meningitidis strain IM2169- or IM2394-related
XX transferrin Tbp2 subunit homologous to one of the epitope sequences
XX YKGTW, EEFYDFSDTKTKTL, EGGEYGPKGSEL or AVFGAK (AAR8663-R88666)
XX from N.meningitidis strain IM2394 and cannot recognise an epitope in
XX the third domain.
XX
SQ Sequence 6 AA;

Query Match 100.0%; Score 15; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 7.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
   |||
Db 3 KGA 5

endothelin function
|||
1 KGA 3

Db 3 KGA 5

RESULT 16
AAY39235
ID AAY39235 standard; peptide; 6 AA.
XX
AC AAY39235;
XX
XX 23-NOV-1999 (first entry)
XX
XX
XX Cyclic peptide used to inhibit p75-NTR mediated apoptosis.
XX
XX Cyclic peptide; p75NTR; p75 neurotrophin receptor; nerve growth factor;
XX NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; beta-amyloid;
XX Alzheimer's disease; pseudo-ligand; hair growth; hair colour;
XX skin colour; alopecia areata; male pattern baldness.

```


CC cellular condition achievable by application of staurosporine, and
 CC diseases responsive to inhibition of a cellular condition achievable by
 CC application of staurosporine. The diseases include neurodegenerative
 CC diseases, neuropathies, immunodeficiencies, geriatric disease, transplant
 CC rejection diseases, hyperproliferative diseases, autoimmune diseases and
 CC dermatological diseases.
 XX

SQ Sequence 5 AA;

Query Match 100.0%; Score 15; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 |||
 Db 1 KGA 3

RESULT 7

AAW80207
 ID AAW80207 standard; Peptide; 5 AA.

AC AAW80207;

DT 23-DEC-1998 (first entry)

DE Cleavage site between the leader sequence and VP4 of clone PRMC35.

KW Initiation codons; Lab; leader sequence; Ib;
 KW live recombinant foot-and-mouth disease virus; FMD virus;
 KW active leader proteinase protein; vaccine; immunisation.

XX Synthetic.

XX US5824316-A.

PD 20-OCT-1998.

PF 24-MAY-1996; 96US-0653037.

PR 24-MAY-1996; 96US-0653037.

XX (USDA) US SEC OF AGRIC.

XX Grubman MJ, Mason PW, Piccone ME, Rieder E;

DR WPI; 1998-582501/49.

XX N-PSDB; AAV66361.

PT Live, recombinant foot-and-mouth disease virus - which lacks an
 PT active leader proteinase protein, is useful as a vaccine for
 PT prevention of foot-and-mouth disease

PS Disclosure; Fig 1b; 22pp; English.

XX AAW80205-11 are encoded by wild type and mutant RNAs surrounding the
 CC initiation codons for lab (AAW80205); the polyprotein is positioned
 CC behind the first AUG of the leader sequence, and so live virus is not
 CC generated) and Ib (AAW80206; initiation occurs at the second AUG so that
 CC live virus is produced) and the cleavage site between the leader sequence
 CC and virus protein 4 (VP4) (AAW80207). AAW80208-11 represent mutant
 CC sequences. The sequences are used in the course of the invention to
 CC produce a live, recombinant foot-and-mouth disease (FMD) virus, which
 CC lacks an active leader proteinase protein, the Ib portion of the protein
 CC having been deleted. The mutated virus can be used as a vaccine for
 CC immunisation against FMD.

SQ Sequence 5 AA;

Query Match 100.0%; Score 15; DB 19; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 |||
 Db 2 KGA 4

RESULT 8

AAV39238
 ID AAV39238 standard; peptide; 5 AA.

XX AAV39238;

DT 23-NOV-1999 (first entry)

DE Peptide used for the generation of p75NTR binding peptide.

KW p75NTR; p75 neurotrophin receptor; nerve growth factor;
 KW NGF; melanocyte; keratinocyte; apoptosis; Bcl-2; Alzheimer's disease;
 KW pseudo-ligand; hair growth; hair colour; skin colour; alopecia areata;
 KW male pattern baldness.

XX Synthetic.

XX WO9939728-A2.

PD 12-AUG-1999.

PF 03-FEB-1999; 99WO-US02362.

PR 04-FEB-1998; 98US-0018194.

XX (UYBO-) UNIV BOSTON.

XX Eller M, Gilchrest BA, Yaar M;

XX WPI; 1999-539950/45.

PT Controlling or manipulating melanocyte and keratinocyte cell death,
 PT useful for treating, e.g. alopecia areata

PS Disclosure; Page 22; 67pp; English.

XX This sequence is used in the production of a cyclic peptide AAV39235.
 CC The cyclic peptide competes with and competitively inhibits beta-amyloid
 CC binding to the p75 neurotrophin receptor (p75NTR). p75NTR is a low
 CC affinity nerve growth factor (NGF) receptor which is expressed by
 CC melanocytes and keratinocytes of the basal epidermis. Apoptosis can be
 CC inhibited by p75NTR via the upregulation of the Bcl-2 protein. If the
 CC receptor is occupied by appropriate ligands e.g. neurotrophins,
 CC apoptosis is inhibited. Other examples of appropriate ligands include
 CC this cyclic peptide. This peptide is based on the sequence of the binding
 CC fragment of beta-amyloid, which binds to p75NTR in Alzheimer's disease.
 CC This cyclic peptide can be used in methods to control or manipulate
 CC keratinocyte or melanocyte cell death. The methods involve using this
 CC peptide or peptides AAV39234-V39235 to bind as a pseudo-ligand to the p75
 CC neurotrophin receptor, inhibiting apoptosis. The new method can induce or
 CC maintain hair growth, hair colour or skin colour. Inducing or maintaining
 CC hair growth is useful for treating alopecia areata or male pattern
 CC baldness in vertebrates.

SQ Sequence 5 AA;

Query Match 100.0%; Score 15; DB 20; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 |||
 Db 2 KGA 4

RESULT 9

AAW93018
 ID AAW93018 standard; peptide; 5 AA.

OS Synthetic.
 XX JP05078391-A.
 PN 30-MAR-1993.
 PD 12-SEP-1991; 91JP-0232991.
 PF 12-SEP-1991; 91JP-0232991.
 PR 12-SEP-1991; 91JP-0232991.
 XX (HITB) HITACHI CHEM CO LTD.
 PA WPI; 1993-140359/17.
 DR Endothelin-binding peptide comprising 4 or more aminoacid(s) -
 PT useful for detecting endothelin and modifying or inhibiting
 PT endothelin function
 XX Example; Page 5; 8pp; Japanese.
 PS The peptide is capable of binding endothelin or its precursor.
 CC The peptide is useful for determining the presence of endothelin
 CC and as an agent for preventing or inhibiting the action of endothelin.
 CC See also AAR34869-80.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 15; DB 14; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 1 KGA 3
 RESULT 5
 AAW45345
 ID AAW45345 standard; peptide; 5 AA.
 XX
 AC AAW45345;
 XX
 DT 08-MAY-1998 (first entry)
 XX
 DE Peptide used for diagnosing and treating Alzheimer's disease.
 XX
 KW Beta-amyloid; Alzheimer's disease; diagnosis; melanocyte; fragment;
 KW neurotrophin receptor p75; p75NTR; nerve growth factor; NGF.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..5
 FT /note= "Optional disulphide bond"
 XX
 PN W09737228-A1.
 XX
 PD 09-OCT-1997.
 XX
 PF 28-MAR-1997; 97WO-US04966.
 XX
 PR 29-MAR-1996; 96US-0625765.
 XX
 PA (UYBO-) UNIV BOSTON.
 XX
 XX Gilchrist BA, Yaar M;
 PI WPI; 1997-512306/47.
 DR
 XX Evaluating risk of individual to develop Alzheimer's - uses cultured
 XX epidermal melanocyte(s), also useful for developing therapies for
 PT neuro-degenerative diseases

XX Disclosure; Page 21; 42pp; English.
 XX
 CC The invention relates to methods of therapy for Alzheimer's disease
 CC using peptides (AAW45343-6) that bind to the neurotrophin receptor p75
 CC nerve growth factor receptor (NGFR) and competitively inhibit the binding
 CC of a beta-amyloid to the p75 NGFR. Also described is a new method for
 CC evaluating the risk of an individual to develop Alzheimer's disease
 CC using cultured neural crest-derived melanocytes. The methods can be used
 CC for diagnosing and treating Alzheimer's disease and other
 CC neurodegenerative diseases mediated by beta-amyloid protein, or by
 CC aberrant activation of the low affinity NGFR localised on neural cell
 CC surfaces, such as autoimmune encephalomyelitis, Huntington's disease,
 CC cortico-basal degeneration, progressive supra-nuclear palsy,
 CC Gerotman-Straussler Scheinker syndrome, Niemann-Pick disease, and
 CC progressive supranuclear palsy. In the diagnostic tests, the human
 CC melanocytes, which are easily obtainable from skin biopsies, are good
 CC model cells for the study and diagnosis of Alzheimer's disease.
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 15; DB 18; Length 5;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 2 KGA 4
 RESULT 6
 AAW73300
 ID AAW73300 standard; peptide; 5 AA.
 XX
 AC AAW73300;
 XX
 DT 08-FEB-1999 (first entry)
 XX
 DE HL60 cell line protein fragment.
 XX
 KW HL60; human; staurosporine; neurodegenerative disease; neuropathy;
 KW immunodeficiency; geriatric disease; transplant rejection; therapy;
 KW hyperproliferative disease; autoimmune disease; dermatological disease.
 XX
 OS Homo sapiens.
 XX
 PN W09845429-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 14-APR-1998; 98WO-EP02157.
 XX
 PR 10-APR-1997; 97GB-0007307.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Fuerst P, Imfeld D, Maerki W, Schindler P;
 XX
 DR WPI; 1998-568349/48.
 XX
 PT Polypeptides from the HL60 cell line - used to treat
 PT neurodegenerative diseases e.g. neuropathies, immunodeficiencies,
 PT geriatric disease
 XX
 PS Example 7; Page 31; 50pp; English.
 XX
 CC This sequence represents a fragment of a polypeptide of the invention.
 CC The polypeptides were isolated from the HL60 cell line. The polypeptide
 CC can be used as a drug, or as a marker or surrogate marker for monitoring
 CC a cellular condition or disease achievable by application of
 CC staurosporine. They can also be used for identification of a drug for
 CC treatment of a disease selected from disease responsive to induction of a

CC The peptide is useful for determining the presence of endothelin
 CC and as an agent for preventing or inhibiting the action of endothelin.
 CC See also AAR34869-80.

XX Sequence 4 AA;

Query Match 100.0%; Score 15; DB 14; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 |||
 Db 1 KGA 3

RESULT 2

AAAY23842
 ID AAY23842 standard; peptide; 4 AA.

XX AC AAY23842;

XX DT 13-SEP-1999 (first entry)

XX DE Single compound for use in a scaffolded library.

XX KW Substituted cholic acid; scaffold molecule; solid phase synthesis;
 KW mimetic.

XX OS Synthetic.

XX PN WO9931124-A1.

XX PD 24-JUN-1999.

XX PF 11-DEC-1998; 98WO-DK00547.

XX PR 18-DEC-1997; 97US-0068073.

XX PR 12-DEC-1997; 97DK-0001450.

XX PA (NOVO) NOVO-NORDISK AS.

XX PI Hoeg-Jensen T;

XX WPI; 1999-405023/34.

XX PT New cholic acid based scaffolds for multidimensional presentation of
 PT peptides

XX PS Example 2; Page 23; 33pp; English.

XX CC The specification describes substituted cholic acid based scaffold
 CC molecules, prepared by solid phase synthesis. The substituted cholic
 CC acids are prepared by initial solution synthesis of a scaffold folding
 CC amino acids with 3 orthogonal protecting groups. Subsequent solid phase
 CC synthesis provides build up of the target molecules, either as discrete
 CC or in mixture. The molecules may then be screened on the resin or
 CC cleaved from the resin and then screened in solution. The molecules are
 CC potential mimetics of larger peptides. The present sequence
 CC represents a single compound of the invention.

XX Sequence 4 AA;

Query Match 100.0%; Score 15; DB 20; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 |||
 Db 2 KGA 4

RESULT 3

AAE03421

AAE03421 standard; peptide; 4 AA.

XX AAE03421;

XX DT 06-AUG-2001 (first entry)

XX DE Peptide encoded by human antisense oligonucleotide OL-2.

XX KW Human; antisense; amyloid precursor protein; APP; amyloid beta protein;
 KW AbetaP; Alzheimer's disease; cognitive ability; antisense therapy;
 KW nootropic; neuroprotective.

XX OS Homo sapiens.

XX PN WO200142266-A1.

XX PD 14-JUN-2001.

XX PF 08-DEC-2000; 2000WO-US33383.

XX PR 09-DEC-1999; 99US-0458481.

XX PA (UYSL-) UNIV SAINT LOUIS.

XX PI Kumar VB;

XX WPI; 2001-381626/40.

XX N-PSDB; AAD07948.

XX PT Novel antisense compounds for modulating expression of amyloid beta
 PT protein in cells or tissues and for preventing, treating conditions
 PT associated with expression of amyloid beta protein, e.g. Alzheimer's
 PT disease

XX PS Disclosure; Page 68; 70pp; English.

XX CC The present invention relates to an antisense compound comprising
 CC nucleotides complementary to a nucleic acid sequence coding for amyloid
 CC precursor protein (APP) and which inhibits the expression of amyloid
 CC beta protein (Abeta) portion of APP coding sequence while permitting the
 CC expression of at least a portion of APP polynucleotide 5' to the Abeta
 CC portion of APP coding sequence. This antisense compound is useful for
 CC modulating the expression of Abeta in cells or tissues, for preventing
 CC or treating a disease or condition associated with expression of Abeta,
 CC in particular Alzheimer's disease. The antisense compound is also useful
 CC for improving cognitive ability in a mammal having a disease or
 CC condition associated with the expression of Abeta. Antisense compounds
 CC are used in antisense therapy. The present sequence is a peptide
 CC encoded by human antisense oligonucleotide OL-2.

XX Sequence 4 AA;

Query Match 100.0%; Score 15; DB 22; Length 4;
 Best Local Similarity 100.0%; Pred. No. 7.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 |||
 Db 2 KGA 4

RESULT 4

AAR34877

ID AAR34877 standard; peptide; 5 AA.

XX AC AAR34877;

XX DT 18-AUG-1993 (first entry)

XX DE Endothelin binding peptide.

XX KW Precursor; pre endothelin; agent; inhibitor; synthetic.

XX

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 14:03:49 ; Search time 34 Seconds
(without alignments)
11.757 Million cell updates/sec

Title: GUCKER-1

Perfect score: 15

Sequence: 1 kga 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

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Maximum DB seq length: 20

Post-processing: Minimum Match 100%

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	4	AA19871	Endothelin binding
2	15	100.0	4	AA19842	Single compound fo
3	15	100.0	4	AA19842	Peptide encoded by
4	15	100.0	5	AA19877	Endothelin binding
5	15	100.0	5	AA19845	Peptide used for d
6	15	100.0	5	AA198300	HL60 cell line pro
7	15	100.0	5	AA1980207	Cleavage site betw
8	15	100.0	5	AA199238	Peptide used for t
9	15	100.0	5	AA1993018	DE19725619 peptide
10	15	100.0	5	AA199322	Anti-HIV peptide w

11	15	100.0	5	22	AA1964003	Human beta-amyloid
12	15	100.0	5	23	AA1967972	Beta-amyloid p75NR
13	15	100.0	6	14	AA1934869	Endothelin binding
14	15	100.0	6	14	AA1939597	Leukocyte Response
15	15	100.0	6	17	AA1988666	N meningitidis IM2
16	15	100.0	6	20	AA193235	Cyclic peptide use
17	15	100.0	6	20	AA193019	DE19725619 peptide
18	15	100.0	6	20	AA195590	Conopeptide group
19	15	100.0	6	20	AA190100	Rat CART (62-102)
20	15	100.0	6	21	AA1914373	Conopeptide group
21	15	100.0	6	21	AA195764	Inhibiting enteroc
22	15	100.0	6	21	AA195765	Inhibiting enteroc
23	15	100.0	6	21	AA195766	Inhibiting enteroc
24	15	100.0	6	21	AA193399	Consensus sequence
25	15	100.0	6	21	AA193830	Pyrralobenzodiazep
26	15	100.0	6	21	AA193831	Pyrralobenzodiazep
27	15	100.0	6	21	AA195606	Peptide SEQ ID NO:
28	15	100.0	6	22	AA19468	Amino acid sequenc
29	15	100.0	6	23	AA1947138	S chrysomallus act
30	15	100.0	7	16	AA190377	Protein polymeric
31	15	100.0	7	19	AA1972631	Conus genus omega-
32	15	100.0	7	19	AA19762	Lysine donor pepti
33	15	100.0	7	20	AA193020	DE19725619 peptide
34	15	100.0	7	23	AA1947140	S chrysomallus act
35	15	100.0	7	23	AA1947142	S chrysomallus act
36	15	100.0	8	14	AA1937284	PM-1/BSA peptide.
37	15	100.0	8	14	AA1937285	PM-1/BSA peptide.
38	15	100.0	8	14	AA1937286	PM-1/BSA peptide.
39	15	100.0	8	14	AA1937287	PM-1/BSA peptide.
40	15	100.0	8	17	AA197226	HIV-1 group O stra
41	15	100.0	8	18	AA1945343	Beta-amyloid fragm
42	15	100.0	8	19	AA1957531	Molecular mimetic
43	15	100.0	8	20	AA1939236	Beta-amyloid fragm
44	15	100.0	8	20	AA193021	DE19725619 peptide
45	15	100.0	8	20	AA193022	DE19725619 peptide

ALIGNMENTS

RESULT 1
AA1934871
ID AA1934871 standard; peptide; 4 AA.
XX
AC AA1934871;
XX
DT 18-AUG-1993 (first entry)
XX
DE Endothelin binding peptide.
XX
KW Precursor; pre endothelin; agent; inhibitor; synthetic.
XX
OS Synthetic.
XX
PN JP05078391-A.
XX
PD 30-MAR-1993.
XX
PF 12-SEP-1991; 91JP-0232991.
XX
PR 12-SEP-1991; 91JP-0232991.
XX
PA (HITB) HITACHI CHEM CO LTD.
XX
DR WPI; 1993-140359/17.
XX
PT Endothelin-binding peptide comprising 4 or more aminoacid(s) -
PT useful for detecting endothelin and modifying or inhibiting
PT endothelin function
XX
PS Example; Page 5; 8pp; Japanese.
XX
CC The peptide is capable of binding endothelin or its precursor.

; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence from
; OTHER INFORMATION: a phage display peptide library
US-08-925-002-40

Query Match 100.0%; Score 15; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 3 KGA 5

RESULT 43

US-09-163-095-4
; Sequence 4, Application US/09163095
; Patent No. 6242416
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE OF INVENTION: ALZHEIMER'S DISEASE
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/163,095
; CURRENT FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: PCT/US97/04966
; EARLIER FILING DATE: 1997-03-28
; EARLIER APPLICATION NUMBER: 08/625,765
; EARLIER FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
US-09-163-095-4

Query Match 100.0%; Score 15; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 6 KGA 8

RESULT 44

US-09-001-984C-13
; Sequence 13, Application US/09001984C
; Patent No. 6245331
; GENERAL INFORMATION:
; APPLICANT: Laal, Suman
; APPLICANT: Zolla-Pazner, Susan
; APPLICANT: Belisle, John T
; TITLE OF INVENTION: EARLY DETECTION OF MYCOBACTERIAL DISEASE
; FILE REFERENCE: NYU-011
; CURRENT APPLICATION NUMBER: US/09/001,984C
; CURRENT FILING DATE: 1997-12-31
; PRIOR APPLICATION NUMBER: 60/034,003
; PRIOR FILING DATE: 1996-12-31
; NUMBER OF SEQ ID NOS: 106
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis strain H37Rv
US-09-001-984C-13

Query Match 100.0%; Score 15; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 6 KGA 8

RESULT 45

US-09-097-194-14
; Sequence 14, Application US/09097194
; Patent No. 6359112
; GENERAL INFORMATION:
; APPLICANT: Kapurniotu, Afroditi
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: Peptides Used As Agonists And/Or Inhibitors Of Amyloid
; TITLE OF INVENTION: Formation And Cytotoxicity And Also For Use In
; TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
; TITLE OF INVENTION: In Spongiform Encephalopathies
; FILE REFERENCE: US 09/097,194
; CURRENT APPLICATION NUMBER: US/09/097,194
; CURRENT FILING DATE: 1998-06-12
; EARLIER APPLICATION NUMBER: DE 197 25 619.8
; EARLIER FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-097-194-14

Query Match 100.0%; Score 15; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 4 KGA 6

Search completed: November 9, 2002, 14:13:48
Job time : 15 secs

Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 1 KGA 3
Db 6 KGA 8

RESULT 40

US-08-159-339A-835
; Sequence 835, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 835:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-835

Query Match 100.0%; Score 15; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 1 KGA 3
Db 4 KGA 6

RESULT 41

US-08-159-339A-846
; Sequence 846, Application US/08159339A
; Patent No. 6037135

; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-005030US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 846:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-846

Query Match 100.0%; Score 15; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 0;

Qy 1 KGA 3
Db 7 KGA 9

RESULT 42

US-08-925-002-40
; Sequence 40, Application US/08925002
; Patent No. 6048527
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan M.
; APPLICANT: Moe, Gregory R.
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 1238,002
; CURRENT APPLICATION NUMBER: US/08/925,002
; CURRENT FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
;; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
;; CITY: SAN FRANCISCO
;; STATE: CALIFORNIA
;; COUNTRY: U.S.A.
;; ZIP: 94111
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/633,148
;; FILING DATE: 16-APR-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: MURPHY ESQ., MATTHEW B.
;; REGISTRATION NUMBER: 39,787
;; REFERENCE/DOCKET NUMBER: 014618-005600US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 326-2400
;; TELEFAX: (415) 326-2422
;; INFORMATION FOR SEQ ID NO: 13:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-633-148-13

Query Match 100.0%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 2 KGA 4

RESULT 38
US-08-713-636-3
;; Sequence 3, Application US/08/13636
;; Patent No. 5942415
;; GENERAL INFORMATION:
;; APPLICANT: Schraven, B. et al.
;; TITLE OF INVENTION: SKAP55 Compositions and Methods of Use Therefor
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: LAHIVE & COCKFIELD
;; STREET: 60 State Street, suite 510
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02109-1875
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent in Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/713,636
;; FILING DATE: 13-APR-1994
;; CLASSIFICATION: 530
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US
;; FILING DATE: Herewith
;; ATTORNEY/AGENT INFORMATION:
;; NAME: DeConti, Giulio A.
;; REGISTRATION NUMBER: 31,503
;; REFERENCE/DOCKET NUMBER: BBI-066
;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (617)227-7400
;; TELEFAX: (617)227-5941
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; FRAGMENT TYPE: internal
;; US-08-713-636-3

Query Match 100.0%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 1 KGA 3

RESULT 39
US-08-159-339A-794
;; Sequence 794, Application US/08159339A
;; Patent No. 6037135
;; GENERAL INFORMATION:
;; APPLICANT: Kubo, Ralph T.
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Celis, Esteban
;; TITLE OF INVENTION: HLA Binding peptides and Their
;; NUMBER OF SEQUENCES: 1254
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: CA
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/159,339A
;; FILING DATE: 29-NOV-1993
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/926,666
;; FILING DATE: 07-AUG-1992
;; APPLICATION NUMBER: US 08/027,746
;; FILING DATE: 05-MAR-1993
;; APPLICATION NUMBER: US 08/103,396
;; FILING DATE: 06-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weber, Ellen Lauver
;; REGISTRATION NUMBER: 32,762
;; REFERENCE/DOCKET NUMBER: 018623-005030US
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 576-0200
;; TELEFAX: (415) 576-0300
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 794:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-159-339A-794

Query Match 100.0%; Score 15; DB 3; Length 10;

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; TITLE OF INVENTION: 29 Human Secreted Proteins
; FILE REFERENCE: P2015P1
; CURRENT APPLICATION NUMBER: US/09/257,179
; EARLIER FILING DATE: 1999-02-25
; EARLIER APPLICATION NUMBER: PCT/US98/17709
; EARLIER FILING DATE: 1998-08-27
; EARLIER APPLICATION NUMBER: 60/056,270
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,271
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,247
; EARLIER FILING DATE: 1997-08-29
; EARLIER APPLICATION NUMBER: 60/056,073
; EARLIER FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; TYPE: PRT
; LENGTH: 9
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-09-257-179-112

Query Match      100.0%; Score 15; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
Db      6 KGA 8

RESULT 35
US-08-750-007-8
; Sequence 8, Application US/08750007
; Patent No. 5801016
; GENERAL INFORMATION:
; APPLICANT: MORIOKA, SHINJI
; APPLICANT: UKI, JUN
; TITLE OF INVENTION: DNA FRAGMENT, RECOMBINANT VECTOR
; TITLE OF INVENTION: CONTAINING THE SAME AND METHOD FOR EXPRESSING FOREIGN
; TITLE OF INVENTION: GENES USING THE SAME
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
; STREET: PO BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,007
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 0760-221P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 205-8000
; TELEFAX: (703) 205-8050
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-750-007-8

Query Match      100.0%; Score 15; DB 15; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
Db      3 KGA 5

RESULT 36
US-08-633-148-5
; Sequence 5, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSENT & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESQ., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-633-148-5

Query Match      100.0%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
Db      2 KGA 4

RESULT 37
US-08-633-148-13
; Sequence 13, Application US/08633148
; Patent No. 5864018
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
```


; TITLE OF INVENTION: HLA Binding peptides and Their
; Uses
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Fast-Seq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 817:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-817

Query Match 100.0%; Score 15; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 1 KGA 3

RESULT 32
US-08-471-586-6
; Sequence 6, Application US/08471586
; Patent No. 6080407
; GENERAL INFORMATION:
; APPLICANT: Bucala, Richard J. et al.
; TITLE OF INVENTION: Inhibition of Migration Inhibitory Factor in the Treatment of
; TITLE OF INVENTION: Cytokine-Mediated Toxicity
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PICOWER INSTITUTE FOR MEDICAL RESEARCH
; STREET: 350 Community Drive
; CITY: Manhasset
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11030
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: Word

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,586
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Oster, Jeffrey B.
; REGISTRATION NUMBER: 32,585
; REFERENCE/DOCKET NUMBER: 0203G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516 562 9404
; TELEFAX: 516 365 7919
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-586-6

Query Match 100.0%; Score 15; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 3 KGA 5

RESULT 33
US-09-202-832-8
; Sequence 8, Application US/09202832
; Patent No. 6194190
; GENERAL INFORMATION:
; APPLICANT: IZO, Yukiko
; APPLICANT: TANAKA, Tetsuki
; APPLICANT: MIYAGI, Masaru
; APPLICANT: TANIGAWA, Tetsuo
; APPLICANT: TOMONO, Jun
; APPLICANT: TSUNASAWA, Susumu
; APPLICANT: KATO, Ikunoshin
; TITLE OF INVENTION: NOVEL AMINO-TERMINAL DEBLOCKING ENZYME
; FILE REFERENCE: 1422-368P
; CURRENT APPLICATION NUMBER: US/09/202,832
; CURRENT FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: manufactured
; OTHER INFORMATION: by BACHEM
US-09-202-832-8

Query Match 100.0%; Score 15; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 4 KGA 6

RESULT 34
US-09-257-179-112
; Sequence 112, Application US/09257179
; Patent No. 6410709
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

```
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-471-546-1

Query Match 100.0%; Score 15; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 3 KGA 5

RESULT 29
US-08-159-339A-792
; Sequence 792, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 792:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-792

Query Match 100.0%; Score 15; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 3 KGA 5

RESULT 30
US-08-159-339A-805
; Sequence 805, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: HLA Binding peptides and Their
; NUMBER OF SEQUENCES: 1254
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/159,339A
; FILING DATE: 29-NOV-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/926,666
; FILING DATE: 07-AUG-1992
; APPLICATION NUMBER: US 08/027,746
; FILING DATE: 05-MAR-1993
; APPLICATION NUMBER: US 08/103,396
; FILING DATE: 06-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 018623-0050300S
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX:
; INFORMATION FOR SEQ ID NO: 805:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-159-339A-805

Query Match 100.0%; Score 15; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 6 KGA 8

RESULT 31
US-08-159-339A-817
; Sequence 817, Application US/08159339A
; Patent No. 6037135
; GENERAL INFORMATION:
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Sette, Alessandro
; APPLICANT: Celis, Esteban
```

QY 1 KGA 3
111
Db 4 KGA 6

RESULT 26

US-09-097-194-13
; Sequence 13, Application US/09097194
; Patent No. 6359112
; GENERAL INFORMATION:
; APPLICANT: Kapuriotu, Afroditi
; APPLICANT: Bernhagen, Juergen
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: Peptides Used As Agonists And/Or Inhibitors Of Amyloid
; TITLE OF INVENTION: Formation And Cytotoxicity And Also For Use In
; TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
; TITLE OF INVENTION: In Spongiform Encephalopathies
; FILE REFERENCE: US 09/097,194
; CURRENT FILING DATE: 1998-06-12
; EARLIER APPLICATION NUMBER: DE 197 25 619.8
; EARLIER FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-097-194-13

Query Match 100.0%; Score 15; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
111
Db 2 KGA 4

RESULT 27

US-08-817-441-24
; Sequence 24, Application US/08817441
; Patent No. 6399294
; GENERAL INFORMATION:
; APPLICANT: CHARNEAU, PIERRE
; APPLICANT: CLAVEL, FRANCOISE
; APPLICANT: BORMAN, ANDREW
; APPLICANT: QUILLIENT, CAROLINE
; APPLICANT: GUETARD, DENISE
; APPLICANT: MONTAGNIER, LUC
; APPLICANT: DONTON DE SAINT-MARTIN, JACQUELINE
; APPLICANT: COHEN, JACQUES
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF HIV-1 TYPE (OR
; TITLE OF INVENTION: SUBTYPE) ANTIGENS
; NUMBER OF SEQUENCES: 103
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/817,441
; FILING DATE: 11-JUL-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR 95/01391

; FILING DATE: 20-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9412554
; FILING DATE: 20-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 9502526
; FILING DATE: 03-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyers, Kenneth J.
; REGISTRATION NUMBER: 25,146
; REFERENCE/DOCKET NUMBER: 03260.6005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-817-441-24

Query Match 100.0%; Score 15; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
111
Db 5 KGA 7

RESULT 28

US-08-471-546-1
; Sequence 1, Application US/08471546
; Patent No. 6030615
; GENERAL INFORMATION:
; APPLICANT: Bucala, Richard J.
; APPLICANT: Mitchell, Robert A.
; APPLICANT: Bernhagen, Juergen
; APPLICANT: Calandra, Thierry F.
; APPLICANT: Cerami, Anthony P.
; TITLE OF INVENTION: INHIBITION OF MIGRATION INHIBITORY
; TITLE OF INVENTION: FACTOR IN THE TREATMENT OF DISEASES INVOLVING
; TITLE OF INVENTION: CYTOKINE-MEDIATED TOXICITY
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,546
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7815-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids

```
Db          3 KGA 5

Query Match          100.0%; Score 15; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 KGA 3
           111
Db          3 KGA 5

RESULT 24
US-09-163-095-1
; Sequence 1, Application US/09163095
; Patent No. 6242416
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/163,095
; CURRENT FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: PCT/US97/04966
; EARLIER FILING DATE: 1997-03-28
; EARLIER APPLICATION NUMBER: 08/625,765
; EARLIER FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-163-095-1

Query Match          100.0%; Score 15; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 KGA 3
           111
Db          5 KGA 7

RESULT 25
US-09-097-194-12
; Sequence 12, Application US/09097194
; Patent No. 6359112
; GENERAL INFORMATION:
; APPLICANT: Kapurniotu, Afroditi
; APPLICANT: Bernhagen, Juergen
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: Peptides Used As Agonists And/Or Inhibitors Of Amyloid
; TITLE OF INVENTION: Formation And Cytotoxicity And Also For Use In
; TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
; TITLE OF INVENTION: In Spongiform Encephalopathies
; FILE REFERENCE: US 09/097,194
; CURRENT APPLICATION NUMBER: US/09/097,194
; CURRENT FILING DATE: 1998-06-12
; EARLIER APPLICATION NUMBER: DE 197 25 619.8
; EARLIER FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-097-194-12

Query Match          100.0%; Score 15; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 KGA 3
           111
Db          1 KGA 3

RESULT 23
US-08-925-002-31
; Sequence 31, Application US/08925002
; Patent No. 6048527
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan M.
; APPLICANT: Moe, Gregory R.
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 1238.002
; CURRENT APPLICATION NUMBER: US/08/925,002
; CURRENT FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence from
; OTHER INFORMATION: a phage display peptide library

US-08-925-002-31
; Sequence 31, Application PC/TUS9503239
; Patent No. 6048527
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03239
; FILING DATE: 14-MAR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/212,433
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: farnelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-2PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US95-03239-27

Query Match          100.0%; Score 15; DB 5; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 KGA 3
           111
Db          1 KGA 3

RESULT 23
US-08-925-002-31
; Sequence 31, Application US/08925002
; Patent No. 6048527
; GENERAL INFORMATION:
; APPLICANT: Granoff, Dan M.
; APPLICANT: Moe, Gregory R.
; TITLE OF INVENTION: USE OF MONOCLONAL ANTIBODIES THAT DEFINE UNIQUE
; TITLE OF INVENTION: MENINGOCOCCAL B EPITOPES IN THE PREPARATION OF VACCINE
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 1238.002
; CURRENT APPLICATION NUMBER: US/08/925,002
; CURRENT FILING DATE: 1997-08-27
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: sequence from
; OTHER INFORMATION: a phage display peptide library
```

;
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-212-433A-27

Query Match 100.0%; Score 15; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 1 KGA 3

RESULT 19
US-08-397-633A-96
; Sequence 96, Application US/08397633A
; Patent No. 5773577
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; TITLE OF INVENTION: PRODUCTS COMPRISING SUBSTRATESCAPABLE
; TITLE OF INVENTION: OF ENZYMATIC CROSS-LINKING
; NUMBER OF SEQUENCES: 105
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/397,633A
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-58848-1/BIR PROP-011-1
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-397-633A-96

Query Match 100.0%; Score 15; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 5 KGA 7

RESULT 20
US-08-716-256-27
; Sequence 27, Application US/08716256
; Patent No. 6017693
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION

;
; TITLE OF INVENTION: PATTERNS TO IDENTIFY NUCLEOTIDE, AMINO ACID OR
; TITLE OF INVENTION: CARBOHYDRATE SEQUENCES IN DATABASES OR TO IDENTIFY
; TITLE OF INVENTION: ORGANISMS
; NUMBER OF SEQUENCES: 46
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/716,256
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03239
; FILING DATE: 14-MAR-1995
; APPLICATION NUMBER: US 08/212,433
; FILING DATE: 14-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 16336-2PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-467-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-716-256-27

Query Match 100.0%; Score 15; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 1 KGA 3

RESULT 21
US-09-097-194-11
; Sequence 11, Application US/09097194
; Patent No. 6359112
; GENERAL INFORMATION:
; APPLICANT: Kapurniotu, Afroditi
; APPLICANT: Brunner, Herwig
; TITLE OF INVENTION: Peptides Used As Agonists And/Or Inhibitors Of Amyloid
; TITLE OF INVENTION: Formation And Cytotoxicity And Also For Use In
; TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
; TITLE OF INVENTION: In Spongiform Encephalopathies
; FILE REFERENCE: US 09/097,194
; CURRENT APPLICATION NUMBER: US/09/097,194
; CURRENT FILING DATE: 1998-06-12
; EARLIER APPLICATION NUMBER: DE 197 25 619.8
; EARLIER FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-097-194-11

Query Match 100.0%; Score 15; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3

REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE 32
INDIVIDUAL ISOLATE: 32
US-09-392-979A-22

Query Match 100.0%; Score 15; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
DB 4 KGA 6

RESULT 16
US-09-097-194-10
Sequence 10, Application US/09097194
Patent No. 6359112
GENERAL INFORMATION:
APPLICANT: Kapuriotu, Afroditi
APPLICANT: Brunner, Juergen
TITLE OF INVENTION: Peptides Used As Agonists And/Or Inhibitors Of Amyloid
TITLE OF INVENTION: Formation And Cytotoxicity And Also For Use In
TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
TITLE OF INVENTION: In Spongiform Encephalopathies
FILE REFERENCE: US 09/097,194
CURRENT APPLICATION NUMBER: US/09/097,194
CURRENT FILING DATE: 1998-06-12
EARLIER APPLICATION NUMBER: DE 197 25 619.8
EARLIER FILING DATE: 1997-06-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 6
TYPE: PRT
ORGANISM: Homo sapiens
US-09-097-194-10

Query Match 100.0%; Score 15; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
DB 2 KGA 4

RESULT 17
US-07-866-678-6
Sequence 6, Application US/07866678
Patent No. 5225531
GENERAL INFORMATION:
APPLICANT: Gresham, Hattie D.
APPLICANT: Brown, Eric J.
APPLICANT: Adams, Steven P.
TITLE OF INVENTION: No. 5225531el Hexapeptide
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
STREET: 800 N. Lindbergh

CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/866,678
FILING DATE: 19920409
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Meyer, Scott J.
REGISTRATION NUMBER: 25,275
REFERENCE/DOCKET NUMBER: 07-24(867)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)694-3117
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-866-678-6

Query Match 100.0%; Score 15; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
DB 1 KGA 3

RESULT 18
US-08-212-433A-27
Sequence 27, Application US/08212433A
Patent No. 5538897
GENERAL INFORMATION:
APPLICANT: Yates, III, John R.
APPLICANT: Eng, James K.
TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION
TITLE OF INVENTION: PATTERNS OF PEPTIDES TO IDENTIFY AMINO ACID SEQUENCES IN
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart St. Tower
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,433A
FILING DATE: 14-MAR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Hughes, Richard L.
REGISTRATION NUMBER: 31,264
REFERENCE/DOCKET NUMBER: 16336-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids

;; TITLE OF INVENTION: IMPROVED EPIDURAL
;; TITLE OF INVENTION: METHOD OF PRODUCING ANALGESIA
;; NUMBER OF SEQUENCES: 36
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Dehlinger & Associates
;; STREET: 350 Cambridge Avenue, Suite 250
;; CITY: Palo Alto
;; STATE: CA
;; COUNTRY: US
;; ZIP: 94306-1546
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/613,400A
;; FILING DATE: 08-MAR-1996
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stratford, Carol A.
;; REGISTRATION NUMBER: 34,444
;; REFERENCE/DOCKET NUMBER: 5865-0019
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650-324-0880
;; TELEFAX: 650-324-0960
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT,
;; INDIVIDUAL ISOLATE: PAGE 33, LINES 16-28
US-08-613-400A-22

Query Match 100.0%; Score 15; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGA 3
|||
Db 4 KGA 6

RESULT 14
US-09-298-017-22
; Sequence 22, Application US/09298017
; Patent No. 6087091
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/298,017
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/049,794
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Stratford, Carol A.
;; REGISTRATION NUMBER: 34,444
;; REFERENCE/DOCKET NUMBER: 5865-0009.30
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 324-0880
;; TELEFAX: (415) 324-0960
;; INFORMATION FOR SEQ ID NO: 22:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 6 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; HYPOTHETICAL: NO
;; ORIGINAL SOURCE:
;; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
;; INDIVIDUAL ISOLATE: 32
US-09-298-017-22

Query Match 100.0%; Score 15; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGA 3
|||
Db 4 KGA 6

RESULT 15
US-09-392-979A-22
; Sequence 22, Application US/09392979A
; Patent No. 6136786
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; TITLE OF INVENTION: ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/392,979A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.

; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
; INDIVIDUAL ISOLATE: 32
US-08-675-354-22

Query Match 100.0%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 4 KGA 6

RESULT 11
US-08-965-918-22
; Sequence 22, Application US/08965918
; Patent No. 5891849
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND FORMULATIONS FOR PREVENTING
; PROGRESSION OF NEUROPATHIC PAIN
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94306-1546
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/965,918
; FILING DATE: 07-NOV-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mohr, Judy M.
; REGISTRATION NUMBER: 38,563
; REFERENCE/DOCKET NUMBER: 5865-0009.34
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT

Query Match 100.0%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 4 KGA 6

RESULT 12
US-09-138-439-22
; Sequence 22, Application US/09138439
; Patent No. 5994305
; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAPEN L
; APPLICANT: MILANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; ENHANCING OPIATE ANALGESIA
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/138,439
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 1993-04-15
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
; INDIVIDUAL ISOLATE: 32
US-09-138-439-22

Query Match 100.0%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 4 KGA 6

RESULT 13
US-08-613-400A-22
; Sequence 22, Application US/08613400A
; Patent No. 6054429
; GENERAL INFORMATION:
; APPLICANT: Bowersox, S. Scott
; APPLICANT: Gadbois, Theresa
; APPLICANT: Pettus, Mark, R.
; APPLICANT: Luther, Robert, R.

STATE: CA
COUNTRY: US
ZIP: 94306-1546
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,847
FILING DATE: 27-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0960
TELEFAX: 650-324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT
US-08-496-847-22

Query Match 100.0%; Score 15; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KGA 3
|||
Db 4 KGA 6

RESULT 9
US-08-742-774-22
Sequence 22, Application US/08/42774
Patent No. 5824645
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/742,774
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/675,354
FILING DATE: 03-JUL-1996
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15

APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
INDIVIDUAL ISOLATE: 32
US-08-742-774-22

Query Match 100.0%; Score 15; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05; Indels 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

QY 1 KGA 3
|||
Db 4 KGA 6

RESULT 10
US-08-675-354-22
Sequence 22, Application US/08675354
Patent No. 5859186
GENERAL INFORMATION:
APPLICANT: JUSTICE, ALAN
APPLICANT: SINGH, TEJINDER
APPLICANT: GOHIL, KISHOR C
APPLICANT: VALENTINO, KAREN L
APPLICANT: MILJANICH, GEORGE P
TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Law Offices of Peter Dehlinger
STREET: 350 Cambridge Avenue, Suite 300
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,354
FILING DATE: 03-JUL-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/049,794
FILING DATE: 1993-APR-15
APPLICATION NUMBER: US 07/814,759
FILING DATE: 30-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stratford, Carol A.
REGISTRATION NUMBER: 34,444
REFERENCE/DOCKET NUMBER: 5865-0009.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:

QY 1 KGA 3
|||
Db 1 KGA 3

RESULT 6

US-07-789-913-22
; Sequence 22, Application US/07789913
; Patent No. 5559095
; GENERAL INFORMATION:
; APPLICANT: Miljanich, George P.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Fox, James A.
; APPLICANT: Valentino, Karen L.
; APPLICANT: Bitner, Robert S.
; APPLICANT: Yamashiro, Donald H.
; TITLE OF INVENTION: Delayed Treatment Method of Reducing
; NUMBER OF INVENTION: Ischemia-Related Neuronal Damage
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/789,913
; FILING DATE: 19911112
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/561,766
; FILING DATE: 02-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/440,094
; FILING DATE: 22-NOV-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0005.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: both
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: peptide fragment used in the claims
US-07-789-913-22

Query Match 100.0%; Score 15; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 4 KGA 6

RESULT 7

US-08-049-794-22
; Sequence 22, Application US/08049794
; Patent No. 5587454

; GENERAL INFORMATION:
; APPLICANT: JUSTICE, ALAN
; APPLICANT: SINGH, TEJINDER
; APPLICANT: GOHIL, KISHOR C
; APPLICANT: VALENTINO, KAREN L
; APPLICANT: MILJANICH, GEORGE P
; TITLE OF INVENTION: METHODS OF PRODUCING ANALGESIA AND
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Law Offices of Peter Dehlinger
; STREET: 350 Cambridge Avenue, Suite 300
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/049,794
; FILING DATE: 19930415
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/814,759
; FILING DATE: 30-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Stratford, Carol A.
; REGISTRATION NUMBER: 34,444
; REFERENCE/DOCKET NUMBER: 5865-0009.30
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 324-0880
; TELEFAX: (415) 324-0960
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE: CONOPEPTIDE GROUP 1 FRAGMENT, PAGE
; INDIVIDUAL ISOLATE: 32
US-08-049-794-22

Query Match 100.0%; Score 15; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 4 KGA 6

RESULT 8

US-08-496-847-22
; Sequence 22, Application US/08496847
; Patent No. 5795864
; GENERAL INFORMATION:
; APPLICANT: Amstutz, Gary A.
; APPLICANT: Bowersox, Stephen S.
; APPLICANT: Gohil, Kishorchandra
; APPLICANT: Adriaenssens, Peter I.
; APPLICANT: Kristipati, Ramasharma
; TITLE OF INVENTION: METHODS AND
; NUMBER OF INVENTION: FORMULATIONS FOR PREVENTING PROGRESSION OF NEUROPATHIC PAIN
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dehlinger & Associates
; STREET: 350 Cambridge Avenue, Suite 250
; CITY: Palo Alto

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/653,037A
; FILING DATE: 24-MAY-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Graeter, Janelle S.
; REGISTRATION NUMBER: 35,024
; REFERENCE/DOCKET NUMBER: 0007.95
; TELEPHONE: 301-504-5060
; TELEFAX: 301-504-5060
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-653-037A-6

Query Match 100.0%; Score 15; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGA 3
Db 2 KGA 4

RESULT 3
US-09-163-095-3
; Sequence 3, Application US/09163095
; Patent No. 6242416
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/163,095
; CURRENT FILING DATE: 1998-09-29
; EARLIER APPLICATION NUMBER: PCT/US97/04966
; EARLIER FILING DATE: 1997-03-28
; EARLIER APPLICATION NUMBER: 08/625,765
; EARLIER FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
; US-09-163-095-3

Query Match 100.0%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGA 3
Db 2 KGA 4

RESULT 4
US-09-097-194-9
; Sequence 9, Application US/09097194
; Patent No. 6359112
; GENERAL INFORMATION:
; APPLICANT: Kapuriotu, Afroditi
; APPLICANT: Bernhagen, Juergen
; TITLE OF INVENTION: Peptides Used As Agonists And/Or Inhibitors Of Amyloid
; TITLE OF INVENTION: Formation And Cytotoxicity And Also For Use In
; TITLE OF INVENTION: Alzheimers Disease, In Type II Diabetes Mellitus And
; TITLE OF INVENTION: In Spongiform Encephalopathies
; FILE REFERENCE: US 09/097,194
; CURRENT APPLICATION NUMBER: US/09/097,194
; CURRENT FILING DATE: 1998-06-12
; EARLIER APPLICATION NUMBER: DE 197 25 619.8
; EARLIER FILING DATE: 1997-06-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-097-194-9

Query Match 100.0%; Score 15; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KGA 3
Db 1 KGA 3

RESULT 5
US-07-866-678-1
; Sequence 1, Application US/07866678
; Patent No. 5225531
; GENERAL INFORMATION:
; APPLICANT: Gresham, Hattie D.
; APPLICANT: Brown, Eric J.
; APPLICANT: Adams, Steven P.
; TITLE OF INVENTION: No. 5225531el Hexapeptide
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scott J. Meyer, Monsanto Co., A3SG
; STREET: 800 N. Lindbergh
; CITY: St. Louis
; STATE: Missouri
; COUNTRY: USA
; ZIP: 63167
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/866,678
; FILING DATE: 19920409
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Meyer, Scott J.
; REGISTRATION NUMBER: 25,275
; REFERENCE/DOCKET NUMBER: 07-24(867)A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (314)694-3117
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-07-866-678-1

Query Match 100.0%; Score 15; DB 1; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

Run on: November 9, 2002, 14:11:40 ; Search time 14 Seconds
(without alignments)
6.305 Million cell updates/sec

Title: GUCKER-1

Perfect score: 15

Sequence: 1 kga 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 184

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	15	100.0	4	4	US-09-458-481B-15
2	15	100.0	5	2	US-08-653-037A-6
3	15	100.0	5	4	US-09-163-095-3
4	15	100.0	5	4	US-09-097-194-9
5	15	100.0	6	1	US-07-866-678-1
6	15	100.0	6	1	US-07-789-913-22
7	15	100.0	6	1	US-08-049-794-22
8	15	100.0	6	1	US-08-496-847-22
9	15	100.0	6	2	US-08-742-774-22
10	15	100.0	6	2	US-08-675-354-22
11	15	100.0	6	2	US-08-965-918-22
12	15	100.0	6	2	US-09-138-439-22
13	15	100.0	6	3	US-08-613-400A-22
14	15	100.0	6	3	US-09-288-017-22
15	15	100.0	6	4	US-09-382-979A-22
16	15	100.0	6	4	US-09-097-194-10
17	15	100.0	7	1	US-07-866-678-6
18	15	100.0	7	1	US-08-212-433A-27
19	15	100.0	7	1	US-08-397-633A-96
20	15	100.0	7	3	US-08-716-256-27
21	15	100.0	7	4	US-09-097-194-11
22	15	100.0	7	5	PCT-US95-03239-27
23	15	100.0	8	3	US-08-925-002-31
24	15	100.0	8	4	US-09-163-095-1
25	15	100.0	8	4	US-09-097-194-12
26	15	100.0	8	4	US-09-097-194-13
27	15	100.0	8	4	US-08-817-441-24

28 15 100.0 9 3 US-08-471-546-1 Sequence 1, Appli
29 15 100.0 9 3 US-08-159-339A-792 Sequence 792, App
30 15 100.0 9 3 US-08-159-339A-805 Sequence 805, App
31 15 100.0 9 3 US-08-159-339A-817 Sequence 817, App
32 15 100.0 9 3 US-08-471-586-6 Sequence 6, Appli
33 15 100.0 9 4 US-09-202-832-8 Sequence 8, Appli
34 15 100.0 9 4 US-09-257-179-112 Sequence 112, App
35 15 100.0 10 1 US-08-750-007-8 Sequence 8, Appli
36 15 100.0 10 2 US-08-633-148-5 Sequence 5, Appli
37 15 100.0 10 2 US-08-633-148-13 Sequence 13, Appli
38 15 100.0 10 2 US-08-713-636-3 Sequence 3, Appli
39 15 100.0 10 3 US-08-159-339A-794 Sequence 794, App
40 15 100.0 10 3 US-08-159-339A-835 Sequence 835, App
41 15 100.0 10 3 US-08-159-339A-846 Sequence 846, App
42 15 100.0 10 3 US-08-925-002-40 Sequence 40, Appli
43 15 100.0 10 4 US-09-163-095-4 Sequence 4, Appli
44 15 100.0 10 4 US-09-001-984C-13 Sequence 13, Appli
45 15 100.0 10 4 US-09-097-194-14 Sequence 14, Appli

ALIGNMENTS

RESULT 1
US-09-458-481B-15
; Sequence 15, Application US/09458481B
; Patent No. 6310048
; GENERAL INFORMATION:
; APPLICANT: KUMAR, Vijaya B.
; TITLE OF INVENTION: ANTISENSE MODULATION OF AMYLOID BETA PROTEIN EXPRESSION
; FILE REFERENCE: 16153-9250
; CURRENT APPLICATION NUMBER: US/09/458,481B
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino Acids
; OTHER INFORMATION: Encoded by complement of Antisense Oligonucleotide
; OTHER INFORMATION: of SEQ ID NO:9
US-09-458-481B-15

Query Match 100.0%; Score 15; DB 4; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.9e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
Db 2 KGA 4

RESULT 2
US-08-653-037A-6
; Sequence 6, Application US/08653037A
; Patent No. 5824316
; GENERAL INFORMATION:
; APPLICANT: Grubman, Marvin J.
; APPLICANT: Mason, Peter W.
; APPLICANT: Piccone, Maria E.
; APPLICANT: Rieder, Elizabeth
; TITLE OF INVENTION: Leader-Proteinase Deleted Foot-and-Mouth
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janelle S. Graeter
; STREET: Room 411, Building 005, BARC-W
; CITY: Beltsville
; STATE: MD
; COUNTRY: USA
; ZIP: 20705

; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-67

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 2 KGA 4

RESULT 44
US-09-746-742-68
; Sequence 68, Application US/09746742
; Patent No. US2002007284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 18
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-68

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 2 KGA 4

RESULT 45
US-09-520-698-4
; Sequence 4, Application US/09520698
; Patent No. US20020128175A1
; GENERAL INFORMATION:
; APPLICANT: Gattadahalli M. Anantharamaiah
; TITLE OF INVENTION: Synthetic Peptides that Enhance LDL Uptake
; FILE REFERENCE: D6084
; CURRENT APPLICATION NUMBER: US/09/520,698
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 09/271,066
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: PEPTIDE
; OTHER INFORMATION: lipid-associating peptide
US-09-520-698-4

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 15 KGA 17

Search completed: November 9, 2002, 14:16:58
Job time : 11 secs

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; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(18)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-746-742-55

Query Match          100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
        |||
Db      2 KGA 4

RESULT 41
US-09-746-742-64
; Sequence 64, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(18)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-746-742-55
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; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-64

Query Match          100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
        |||
Db      2 KGA 4

RESULT 42
US-09-746-742-65
; Sequence 65, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-65

Query Match          100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
        |||
Db      2 KGA 4

RESULT 43
US-09-746-742-67
; Sequence 67, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
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RESULT 37
US-09-746-742-39
; Sequence 39, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR FILING DATE: 1997-04-17
; PRIOR FILING DATE: 1997-04-17
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-39

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 2 KGA 4

RESULT 38
US-09-746-742-40
; Sequence 40, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-40

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 2 KGA 4

RESULT 39
US-09-746-742-41
; Sequence 41, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-41

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 2 KGA 4

RESULT 40
US-09-746-742-55
; Sequence 55, Application US/09746742
; Patent No. US20020077284A1
; GENERAL INFORMATION:

QY 1 KGA 3
|||
Db 16 KGA 18

RESULT 34

US-09-746-742-17
; Sequence 17, Application US/09746742
; Patent No. US20020077284A1

; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.

; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion

; FILE REFERENCE: 0399.1192-008

; CURRENT APPLICATION NUMBER: US/09/746,742

; CURRENT FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: PCT/US99/17351

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: US 60/043,280

; PRIOR FILING DATE: 1997-04-17

; PRIOR APPLICATION NUMBER: US 09/062,241

; PRIOR FILING DATE: 1998-04-17

; PRIOR APPLICATION NUMBER: US 60/094,676

; PRIOR FILING DATE: 1998-07-30

; PRIOR APPLICATION NUMBER: US 60/100,265

; PRIOR FILING DATE: 1998-09-14

; PRIOR APPLICATION NUMBER: US 60/101,058

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/132,295

; PRIOR FILING DATE: 1999-05-03

; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 17

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: D-peptide

US-09-746-742-17

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
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Db 4 KGA 6

RESULT 35

US-09-746-742-19

; Sequence 19, Application US/09746742

; Patent No. US20020077284A1

; GENERAL INFORMATION:

; APPLICANT: Eckert, Deborah M.

; APPLICANT: Chan, David C.

; APPLICANT: Malashkevich, Vladimir

; APPLICANT: Carr, Peter A.

; APPLICANT: Kim, Peter S.

; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion

; FILE REFERENCE: 0399.1192-008

; CURRENT APPLICATION NUMBER: US/09/746,742

; CURRENT FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: PCT/US99/17351

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: US 60/043,280

; PRIOR FILING DATE: 1997-04-17

; PRIOR APPLICATION NUMBER: US 09/062,241

; PRIOR FILING DATE: 1998-04-17

; PRIOR APPLICATION NUMBER: US 60/094,676

; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 19

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: D-peptide

US-09-746-742-19

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 2 KGA 4

RESULT 36

US-09-746-742-38

; Sequence 38, Application US/09746742

; Patent No. US20020077284A1

; GENERAL INFORMATION:

; APPLICANT: Eckert, Deborah M.

; APPLICANT: Chan, David C.

; APPLICANT: Malashkevich, Vladimir

; APPLICANT: Carr, Peter A.

; APPLICANT: Kim, Peter S.

; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion

; FILE REFERENCE: 0399.1192-008

; CURRENT APPLICATION NUMBER: US/09/746,742

; CURRENT FILING DATE: 2000-12-21

; PRIOR APPLICATION NUMBER: PCT/US99/17351

; PRIOR FILING DATE: 1999-07-30

; PRIOR APPLICATION NUMBER: US 60/043,280

; PRIOR FILING DATE: 1997-04-17

; PRIOR APPLICATION NUMBER: US 09/062,241

; PRIOR FILING DATE: 1998-04-17

; PRIOR APPLICATION NUMBER: US 60/094,676

; PRIOR FILING DATE: 1998-07-30

; PRIOR APPLICATION NUMBER: US 60/100,265

; PRIOR FILING DATE: 1998-09-14

; PRIOR APPLICATION NUMBER: US 60/101,058

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/132,295

; PRIOR FILING DATE: 1999-05-03

; NUMBER OF SEQ ID NOS: 68

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 38

; LENGTH: 18

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: D-peptide

US-09-746-742-38

Query Match 100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 2 KGA 4

```

; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-15

Query Match          100.0%; Score 15; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 2 KGA 4

RESULT 31
US-09-746-742-16
; Sequence 16, Application US/09746742
; Patent No. US2002007284A1
; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-16

```

```

Query Match          100.0%; Score 15; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KGA 3
Db 2 KGA 4

```

```

RESULT 32
US-09-746-742-18
; Sequence 18, Application US/09746742
; Patent No. US2002007284A1

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; GENERAL INFORMATION:
; APPLICANT: Eckert, Deborah M.
; APPLICANT: Chan, David C.
; APPLICANT: Malashkevich, Vladimir
; APPLICANT: Carr, Peter A.
; APPLICANT: Kim, Peter S.
; TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
; FILE REFERENCE: 0399.1192-008
; CURRENT APPLICATION NUMBER: US/09/746,742
; CURRENT FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: PCT/US99/17351
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: US 60/043,280
; PRIOR FILING DATE: 1997-04-17
; PRIOR APPLICATION NUMBER: US 09/062,241
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 60/094,676
; PRIOR FILING DATE: 1998-07-30
; PRIOR APPLICATION NUMBER: US 60/100,265
; PRIOR FILING DATE: 1998-09-14
; PRIOR APPLICATION NUMBER: US 60/101,058
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: US 60/132,295
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D-peptide
US-09-746-742-18

```

```

Query Match          100.0%; Score 15; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KGA 3
Db 2 KGA 4

```

```

RESULT 33
US-09-873-459A-44
; Sequence 44, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-44

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Query Match          100.0%; Score 15; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/972,475
FILING DATE: 04-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/617,267
FILING DATE: <Unknown>
APPLICATION NUMBER: USN 08/475,579
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: USN 08/548,998
FILING DATE: 27-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: DeConti, Giulio A.
REGISTRATION NUMBER: 31,503
REFERENCE/DOCKET NUMBER: PPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-972-475-14

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 13 KGA 15

RESULT 28
US-09-996-357-9
Sequence 9, Application US/09996357
Patent No. US20020133001A1
GENERAL INFORMATION:
APPLICANT: Gefter, Malcolm L
APPLICANT: Isreal, David I
APPLICANT: Joyal, John L
APPLICANT: Gosselin, Michael
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR
TREATING AN AMYLOIDOTIC DISEASE
FILE REFERENCE: PPI-105
CURRENT APPLICATION NUMBER: US/09/996,357
CURRENT FILING DATE: 2001-11-27
PRIOR APPLICATION NUMBER: 60/253,302
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/250,198
PRIOR FILING DATE: 2000-11-29
PRIOR APPLICATION NUMBER: 60/257,186
PRIOR FILING DATE: 2000-12-20
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 15
TYPE: PPT
ORGANISM: Homo sapiens
US-09-996-357-9

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 13 KGA 15

RESULT 29
US-09-873-459A-41
Sequence 41, Application US/09873459A
Patent No. US20020064533A1
GENERAL INFORMATION:
APPLICANT: Murray, Kenneth
TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
FILE REFERENCE: A067 CIP
CURRENT APPLICATION NUMBER: US/09/873,459A
PRIOR FILING DATE: 2001-09-17
PRIOR APPLICATION NUMBER: PCT/US99/28755
PRIOR FILING DATE: 1999-12-03
PRIOR APPLICATION NUMBER: 60/110,911
PRIOR FILING DATE: 1998-12-04
NUMBER OF SEQ ID NOS: 47
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41
LENGTH: 16
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (14)
OTHER INFORMATION: bala
OTHER INFORMATION: Description of Artificial Sequence:HBV
OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-41

Query Match 100.0%; Score 15; DB 10; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 10 KGA 12

RESULT 30
US-09-746-742-15
Sequence 15, Application US/09746742
Patent No. US2002007284A1
GENERAL INFORMATION:
APPLICANT: Eckert, Deborah M.
APPLICANT: Chan, David C.
APPLICANT: Malashkevich, Vladimir
APPLICANT: Carr, Peter A.
APPLICANT: Kim, Peter S.
TITLE OF INVENTION: Inhibitors of HIV Membrane Fusion
FILE REFERENCE: 0399,1192-008
CURRENT APPLICATION NUMBER: US/09/746,742
CURRENT FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: PCT/US99/17351
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: US 60/043,280
PRIOR FILING DATE: 1997-04-17
PRIOR APPLICATION NUMBER: US 09/062,241
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: US 60/094,676
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,265
PRIOR FILING DATE: 1998-09-14
PRIOR APPLICATION NUMBER: US 60/101,058

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; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-24

Query Match      100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
Db      13 KGA 15

RESULT 24
US-09-873-459A-25
; Sequence 25, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-25

Query Match      100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
Db      13 KGA 15

RESULT 25
US-09-873-459A-26
; Sequence 26, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC

```

```

; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-26

Query Match      100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
Db      13 KGA 15

RESULT 26
US-09-873-459A-27
; Sequence 27, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-27

Query Match      100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KGA 3
Db      13 KGA 15

RESULT 27
US-09-972-475-14
; Sequence 14, Application US/09972475
; Patent No. US20020098173A1
; GENERAL INFORMATION:
; APPLICANT: Findels, Mark A. et al.
; TITLE OF INVENTION: Modulators of Amyloid Aggregation
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP

```

RESULT 19

US-09-873-459A-20
; Sequence 20, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-20

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 13 KGA 15

RESULT 20

US-09-873-459A-21
; Sequence 21, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 21
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-21

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 13 KGA 15

RESULT 21

US-09-873-459A-22

US-09-873-459A-22
; Sequence 22, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-22

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 13 KGA 15

RESULT 22

US-09-873-459A-23
; Sequence 23, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; PRIOR FILING DATE: 2001-09-17
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1999-12-03
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-23

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 13 KGA 15

RESULT 23

US-09-873-459A-24
; Sequence 24, Application US/09873459A
; Patent No. US20020064533A1

; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-40

Query Match 100.0%; Score 15; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 10 KGA 12

RESULT 15

US-09-873-459A-38
; Sequence 38, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-38

Query Match 100.0%; Score 15; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 10 KGA 12

RESULT 16

US-09-815-248-16
; Sequence 16, Application US/09815248
; Patent No. US20020098540A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; APPLICANT: PENNICA, DIANE
; TITLE OF INVENTION: NOVEL POLYPEPTIDES, AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 10716.36
; CURRENT APPLICATION NUMBER: US/09/815,248
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/191,258
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-09-815-248-16

Query Match 100.0%; Score 15; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 3 KGA 5

RESULT 17

US-09-815-248-20
; Sequence 20, Application US/09815248
; Patent No. US20020098540A1
; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA
; APPLICANT: PENNICA, DIANE
; TITLE OF INVENTION: NOVEL POLYPEPTIDES, AND NUCLEIC ACIDS ENCODING THE SAME
; FILE REFERENCE: 10716.36
; CURRENT APPLICATION NUMBER: US/09/815,248
; CURRENT FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 60/191,258
; PRIOR FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Illustrative
; OTHER INFORMATION: peptide
US-09-815-248-20

Query Match 100.0%; Score 15; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 8 KGA 10

RESULT 18

US-09-865-644-5
; Sequence 5, Application US/09865644
; Patent No. US20020045188A1
; GENERAL INFORMATION:
; APPLICANT: Kamb et al
; TITLE OF INVENTION: METHODS FOR VALIDATING POLYPEPTIDE TARGETS THAT CORRELATE TO
; CELLULAR PHENOTYPES
; FILE REFERENCE: 29345/37561
; CURRENT APPLICATION NUMBER: US/09/865,644
; CURRENT FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Peptide Binder of HPV E6
US-09-865-644-5

Query Match 100.0%; Score 15; DB 10; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
DB 3 KGA 5

; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-9

Query Match 100.0%; Score 15; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 8 KGA 10

RESULT 7
US-09-873-459A-36
; Sequence 36, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-36

Query Match 100.0%; Score 15; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 8 KGA 10

RESULT 8
US-09-873-459A-10
; Sequence 10, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A

; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
US-09-873-459A-10

Query Match 100.0%; Score 15; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 9 KGA 11

RESULT 9
US-09-873-459A-11
; Sequence 11, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV
; OTHER INFORMATION: capsid-binding peptide
; NAME/KEY: MOD_RES
; LOCATION: (11)
; OTHER INFORMATION: bala
US-09-873-459A-11

Query Match 100.0%; Score 15; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
|||
Db 8 KGA 10

RESULT 10
US-09-873-459A-13
; Sequence 13, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A


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; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/866,898
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/163,095
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/625,765
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-898-1

Query Match      100.0%; Score 15; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 5 KGA 7

RESULT 3
US-09-729-835-112
; Sequence 112, Application US/09729835
; Patent No. US20010016847A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 29 Human Secreted Proteins
; FILE REFERENCE: P2015p1
; CURRENT APPLICATION NUMBER: US/09/729,835
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/257,179
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/056,270
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,271
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,247
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,073
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-729-835-112

Query Match      100.0%; Score 15; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 6 KGA 8

RESULT 4
US-09-873-459A-6
; Sequence 6, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
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; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/866,898
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/163,095
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/625,765
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-866-898-1

Query Match      100.0%; Score 15; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 5 KGA 7

RESULT 3
US-09-729-835-112
; Sequence 112, Application US/09729835
; Patent No. US20010016847A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 29 Human Secreted Proteins
; FILE REFERENCE: P2015p1
; CURRENT APPLICATION NUMBER: US/09/729,835
; CURRENT FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: 09/257,179
; PRIOR FILING DATE: 1999-02-25
; PRIOR APPLICATION NUMBER: 60/056,270
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,271
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,247
; PRIOR FILING DATE: 1997-08-29
; PRIOR APPLICATION NUMBER: 60/056,073
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-729-835-112

Query Match      100.0%; Score 15; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 6 KGA 8

RESULT 4
US-09-873-459A-6
; Sequence 6, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
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; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
; TITLE OF INVENTION: COMPONENTS ATTACHED VIA PEPTIDE LIGANDS
; FILE REFERENCE: A067 CIP
; CURRENT APPLICATION NUMBER: US/09/873,459A
; CURRENT FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: PCT/US99/28755
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/110,911
; PRIOR FILING DATE: 1998-12-04
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:HBV capsid
; OTHER INFORMATION: binding peptide
US-09-873-459A-6

Query Match      100.0%; Score 15; DB 10; Length 9;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 7 KGA 9

RESULT 5
US-09-866-898-4
; Sequence 4, Application US/09866898
; Patent No. US20020051988A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrest, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/866,898
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/163,095
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/625,765
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
US-09-866-898-4

Query Match      100.0%; Score 15; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 6 KGA 8

RESULT 6
US-09-873-459A-9
; Sequence 9, Application US/09873459A
; Patent No. US20020064533A1
; GENERAL INFORMATION:
; APPLICANT: Murray, Kenneth
; TITLE OF INVENTION: HBV CORE ANTIGEN PARTICLES WITH MULTIPLE IMMUNOGENIC
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2002, 14:13:30 ; Search time 10 Seconds
(without alignments)
4.326 Million cell updates/sec

Title: GUCKER-1

Perfect score: 15

Sequence: 1 kga 3

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 58

Minimum DB seq length: 3

Maximum DB seq length: 20

Post-processing: Minimum Match 100%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications_AA:*
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3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
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7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	15	100.0	5	10	US-09-866-898-3
2	15	100.0	8	10	US-09-866-898-1
3	15	100.0	9	10	US-09-729-835-112
4	15	100.0	9	10	US-09-873-459A-6
5	15	100.0	10	10	US-09-866-898-4
6	15	100.0	10	10	US-09-873-459A-9
7	15	100.0	10	10	US-09-873-459A-36
8	15	100.0	11	10	US-09-873-459A-10
9	15	100.0	12	10	US-09-873-459A-11
10	15	100.0	12	10	US-09-873-459A-13
11	15	100.0	12	10	US-09-873-459A-18
12	15	100.0	12	10	US-09-873-459A-19
13	15	100.0	12	10	US-09-873-459A-37
14	15	100.0	12	10	US-09-873-459A-40
15	15	100.0	14	10	US-09-873-459A-38
16	15	100.0	14	10	US-09-815-248-16
17	15	100.0	14	10	US-09-815-248-20
18	15	100.0	15	10	US-09-865-644-5
19	15	100.0	15	10	US-09-873-459A-20
20	15	100.0	15	10	US-09-873-459A-21
21	15	100.0	15	10	US-09-873-459A-22
22	15	100.0	15	10	US-09-873-459A-23
23	15	100.0	15	10	US-09-873-459A-24
24	15	100.0	15	10	US-09-873-459A-25
25	15	100.0	15	10	US-09-873-459A-26
26	15	100.0	15	10	US-09-873-459A-27
27	15	100.0	15	10	US-09-972-475-14
28	15	100.0	15	10	US-09-996-357-9
29	15	100.0	15	10	US-09-873-459A-41
30	15	100.0	15	10	US-09-746-742-15
31	15	100.0	15	10	US-09-746-742-16
32	15	100.0	15	10	US-09-746-742-18
33	15	100.0	15	10	US-09-873-459A-44
34	15	100.0	15	10	US-09-746-742-17
35	15	100.0	15	10	US-09-746-742-19
36	15	100.0	15	10	US-09-746-742-38
37	15	100.0	15	10	US-09-746-742-39
38	15	100.0	15	10	US-09-746-742-40
39	15	100.0	15	10	US-09-746-742-41
40	15	100.0	15	10	US-09-746-742-55
41	15	100.0	15	10	US-09-746-742-64
42	15	100.0	15	10	US-09-746-742-65
43	15	100.0	15	10	US-09-746-742-67
44	15	100.0	15	10	US-09-746-742-68
45	15	100.0	15	10	US-09-520-698-4

ALIGNMENTS

RESULT 1

US-09-866-898-3
; Sequence 3, Application US/09866898
; Patent No. US20020051988A1
; GENERAL INFORMATION:
; APPLICANT: Gilchrist, Barbara A.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; FILE OF INVENTION: ALZHEIMER'S DISEASE
; CURRENT FILING DATE: 2001-05-29
; PRIOR FILING DATE: 1996-03-29
; PRIOR APPLICATION NUMBER: US/09/866,898
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/625,765
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
US-09-866-898-3

Query Match 100.0%; Score 15; DB 10; Length 5;
Best Local Similarity 100.0%; Pred. No. 7.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3

DB 2 KGA 4

RESULT 2

US-09-866-898-1
; Sequence 1, Application US/09866898
; Patent No. US20020051988A1
; GENERAL INFORMATION:

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2002, 14:12:55 ; Search time 5 Seconds
(without alignments)
6.757 Million cell updates/sec

Title: GUCKER-1
Perfect score: 15
Sequence: 1 kga 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 39427 seqs, 11261862 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	14	6	US-10-211-088-99 Sequence 99, Appl

SUMMARIES

ALIGNMENTS

RESULT 1
US-10-211-088-99
; Sequence 99, Application US/10211088
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 99
; LENGTH: 14
; TYPE: PRT

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Binding domain
US-10-211-088-99

Query Match 100.0%; Score 15; DB 6; Length 14;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 11 KGA 13

Search completed: November 9, 2002, 14:16:41
Job time : 6 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2002, 14:11:25 ; Search time 28 Seconds
(without alignments)
22.076 Million cell updates/sec

Title: GUCKER-1
Perfect score: 15
Sequence: 1 kga 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 6

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Minimum Match 100%
Maximum Match 100%

Listing first 45 summaries

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5: sp.human:*
6: sp.invertebrate:*
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8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.rodent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	15	100.0	18	2	Q9R7B9 borrelia bu
5	15	100.0	19	3	Q9UR87 candida par
6	15	100.0	20	4	Q9UC56 homo sapien

ALIGNMENTS

RESULT 1
065901
AC 065901: PRELIMINARY: PRT: 11 AA.
DT 01-AUG-1998 (TREMBLrel. 07, Created)

DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Phosphoglucose isomerase (Fragment).
GN PGIC.
OS leavenworthia crassa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Leavenworthia.
OX NCBI_TaxID=70805;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CR8919/CRI5, AND CV. CR8919/CD6;
RA Liu F., Charlesworth D., Kreitman M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF054493; AAC19033.1; -.
DR EMBL: AF054492; AAC19032.1; -.
KW Isomerase.
FT NON_TER 1 1
FT NON_TER 11 11
SQ SEQUENCE 11 AA; 1208 MW; 5026B3A4BDD87337 CRC64;

Query Match 100.0%; Score 15; DB 10; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
DB 5 KGA 7

RESULT 2
P94011
ID P94011
AC P94011: PRELIMINARY: PRT: 12 AA.
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Elongation factor EF-1 alpha A4 (Fragment).
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=GREEN SILIQUES OF A THALIANA ECOTYPE COLUMBIA;
RA Raynal M., Grellet F., laudie M., Meyer Y., Cooke R., Delseny M.;
RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z27066; CAA81582.1; -.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1229 MW; CEDA9EA59422CDD CRC64;

Query Match 100.0%; Score 15; DB 10; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
DB 9 KGA 11

RESULT 3
Q9TRF5
ID Q9TRF5
AC Q9TRF5: PRELIMINARY: PRT: 15 AA.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE Lipid transfer protein (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;

RN [1]
 RP SEQUENCE.
 RX MEDLINE=93320050; PubMed=8329397;
 RA Ko K.W., Oikawa K., Ohnishi T., Kay C.M., Yokoyama S.;
 RT "Purification, characterization, and conformational analysis of rabbit
 RT plasma lipid transfer protein.";
 RL Biochemistry 32:6729-6736(1993).
 SQ SEQUENCE 15 AA; 1581 MW; 6F7FP95A003BA22E3 CRC64;

Query Match 100.0%; Score 15; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 7.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 3 KGA 5

RESULT 4
 Q9R7B9 PRELIMINARY; PRT; 18 AA.
 AC Q9R7B9; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Putative vls recombination cassette Vls14a (Fragment).
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=831;
 RX MEDLINE=97262068; PubMed=9108482;
 RA Zhang J.R., Hargham J.M., Barbour A.G., Norris S.J.;
 RT "Antigenic variation in Lyme disease borreliae by promiscuous
 RT recombination of vlp-like sequence cassettes.";
 RL Cell 89:275-285(1997).
 DR EMBL; U76406; AAC45187.1; -.
 FT NON_TER 1 1
 FT NON_TER 18 18
 SQ SEQUENCE 18 AA; 1841 MW; 3438BELD95E0C7DA CRC64;

Query Match 100.0%; Score 15; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 5 KGA 7

RESULT 5
 Q9UR87 PRELIMINARY; PRT; 19 AA.
 AC Q9UR87; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Class I cytochrome C isoform B (Fragment).
 OS Candida parapsilosis (yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
 OX NCBI_TaxID=5480;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93305688; PubMed=8391313;
 RA Camougrand N., Velours J., Denis M., Guerin M.;
 RT "Isolation, characterization and function of the two cytochromes c of
 RT the yeast Candida parapsilosis.";
 RL Biochim. Biophys. Acta 1143:135-141(1993).
 SQ SEQUENCE 19 AA; 2108 MW; 17023D754FF25F87 CRC64;

Query Match 100.0%; Score 15; DB 3; Length 19;

Best Local Similarity 100.0%; Pred. No. 9.1e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
 DB 11 KGA 13

RESULT 6
 Q9UC56 PRELIMINARY; PRT; 20 AA.
 AC Q9UC56; 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE MSN14 protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96007946; PubMed=7498169;
 RA Giometti C.S., Tollaksen S.L., Chubb C., Williams C., Huberman E.;
 RT "Analysis of proteins from human breast epithelial cells using two-
 RT dimensional gel electrophoresis.";
 RL Electrophoresis 16:1215-1224(1995).
 SQ SEQUENCE 20 AA; 1923 MW; D0574C31688ABAD7 CRC64;

Query Match 100.0%; Score 15; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 9.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KGA 3
 DB 6 KGA 8

Search completed: November 9, 2002, 14:13:27
 Job time : 29 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 14:12:00 ; Search time 15 Seconds
(without alignments)
19.227 Million cell updates/sec

Title: GUCKER-1
Perfect score: 15
Sequence: 1 Kga 3

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 10

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	12	A60528	Insulin-like growth
2	15	100.0	13	PN0048	unidentified QM002
3	15	100.0	14	PT0026	calotropin DI - mu
4	15	100.0	15	PA0087	cytochrome c2 - fu
5	15	100.0	15	A53085	lipid transfer pro
6	15	100.0	16	PH0748	T-cell receptor be
7	15	100.0	18	A24345	Ca ²⁺ -transporting
8	15	100.0	18	B48408	21k high mobility
9	15	100.0	20	A26380	cytochrome P450 4A
10	15	100.0	20	S68617	histone H2A - sea

ALIGNMENTS

RESULT 1
A60528
Insulin-like growth factor-binding protein, serum - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C/Accession: A60528
R:Walton, P.E.; Baxter, R.C.; Burleigh, B.D.; Ethernton, T.D.
Comp. Biochem. Physiol. B 92, 561-567, 1989
A>Title: Purification of the serum acid-stable insulin-like growth factor binding protein
A/Reference number: A60528; PMID:89209787; PMID:2468442
A/Accession: A60528
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-12 <MAL>

Query Match 100.0%; Score 15; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
|||
DB 2 KGA 4

RESULT 2

PN0048
unidentified QM0023 protein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 23-Jan-1998
C/Accession: PN0048
R:Kato, H.
Kawasaki Igakkaiishi 22, 245-259, 1996
A>Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse ne
A/Reference number: PN0041
A/Accession: PN0048
A:Molecule type: protein
A:Residues: 1-13 <KAT>
A:Experimental source: neuroblastoma cell
C/Comment: The molecular mass is 30,500 and the pI is 6.19.
C:Keywords: brain

Query Match 100.0%; Score 15; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
|||
DB 4 KGA 6

RESULT 3

PT0026
calotropin DI - mudar (fragment)
C/Species: Calotropis gigantea (mudar, madar)
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 05-Aug-1994
C/Accession: PT0026
R:Bhattacharya, D.; Sengupta, A.; Sinha, N.K.
Phytochemistry 26, 633-636, 1987
A>Title: Chemical modification and amino terminal sequence of calotropin DI from Calo
A/Reference number: PT0026
A/Accession: PT0026
A:Molecule type: protein
A:Residues: 1-14 <BHA>
C/Comment: This enzyme is classified as a plant cysteine protease.
C:Keywords: pyrrolidone carboxylic acid (Gln) #status experimental
F/I/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 100.0%; Score 15; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
|||
DB 11 KGA 13

RESULT 4

PA0087
cytochrome c2 - fungus (Fusarium sporotrichioides) (fragment)
C/Species: Fusarium sporotrichioides
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C/Accession: PA0087
R:Chow, L.P.; Fukaya, N.; Sugitara, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A>Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotr
A/Reference number: PA0051
A/Accession: PA0087

A:Molecule type: protein
A:Residues: 1-15 <CHO>
C:Keywords: electron transfer; heme; photosynthesis

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
|||
DB 7 KGA 9

RESULT 5

A53085
Lipid transfer protein - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: A53085
R:KO, K.W.; Oikawa, K.; Ohnishi, T.; Kay, C.M.; Yokoyama, S.
Biochemistry 32, 6729-6736, 1993

A:Title: Purification, characterization, and conformational analysis of rabbit plasma 11
A:Reference number: A53085; MUID:93320050; PMID:8329397
A:Accession: A53085

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <KOI>
A:Experimental source: plasma
A>Note: sequence extracted from NCBI backbone (NCBI:P:135263)

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 15;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
|||
DB 3 KGA 5

RESULT 6

PH0748
T-cell receptor beta chain (RA10.3.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0748
R:Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991

A:Title: T cell receptor genes in a series of class I major histocompatibility complex-1
allelic exclusion and antigen-specific repertoire.

A:Reference number: PH0746; MUID:92078846; PMID:1836010

A:Accession: PH0748

A:Molecule type: mRNA

A:Residues: 1-16 <CAS>

A:Cross-references: EMBL:X60839; NID:953883; PIDN:CAA43232.1; PID:953884

A:Experimental source: T lymphocyte

C:Keywords: T-cell receptor

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 16;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
|||
DB 5 KGA 7

RESULT 7

A24345
Ca²⁺-transporting ATPase (EC 3.6.3.8), cardiac muscle - dog (fragment)
C:Species: Canis lupus familiaris (dog)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 19-Apr-2002
A:Accession: A24345

C:Keywords: F.N.; Cable, M.B.; Geisow, M.G.; Green, N.M.

Biochem. Biophys. Res. Commun. 135, 864-869, 1986
A:Title: Primary structure of the nucleotide binding domain of the Ca²⁺-ATPase from
A:Reference number: A24345; MUID:86168850; PMID:2938585

A:Molecule type: protein

A:Residues: 1-18

C:Superfamily: Na⁺/K⁺-transporting ATPase alpha chain; ATPase nucleotide-binding doma
C:Keywords: ATP; cardiac muscle; heart; hydrolase; muscle

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
|||
DB 9 KGA 11

RESULT 8

B48408
21k high mobility group protein, hepatic (isoform 2) - Atlantic salmon (fragment)

C:Species: Salmo salar (Atlantic salmon)

C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 07-Feb-1997

C:Accession: B48408

R:Waters, S.; Khamis, M.; Von Der Decken, A.
Cell. Mol. Biol. 38, 783-789, 1992

A:Title: Purification of the Atlantic salmon hepatic 21 kDa protein and classificatio

A:Reference number: A48408

A:Accession: B48408

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <MAT>

C:Keywords: liver

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 18;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
|||
DB 4 KGA 6

RESULT 9

A26380
cytochrome P450 4A2 - rat (fragment)

N:Alternate names: cytochrome P450K-5

C:Species: Rattus norvegicus (Norway rat)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 05-Mar-1999

C:Accession: A26380

R:Imaoka, S.; Funae, Y.
Biochem. Biophys. Res. Commun. 141, 711-717, 1986

A:Title: Purification and NH₂-terminal sequence of cytochrome P-450 from kidney micro

A:Reference number: A26380; MUID:87100198; PMID:3801020

A:Accession: A26380

A:Molecule type: protein

A:Residues: 1-20 <IMA>

A:Experimental source: kidney, untreated rats

R:Kimura, S.; Hardwick, J.P.; Kozak, C.A.; Gonzalez, F.J.
DNA 8, 517-525, 1989

A:Title: The rat clotribate-inducible CYP4A subfamily II. cDNA sequence of IVA3, mapp

A:Reference number: A32966; MUID:89356272; PMID:2766933

A:Contents: annotation; identification of constitutive kidney form as CYP4A2

C:Genetics:

A:Gene: CYP4A2

A:Superfamily: human cytochrome P450 CYP4B1, cytochrome P450 homology

C:Keywords: electron transfer; heme; monooxygenase; oxidoreductase; transmembrane pro

Query Match
Best Local Similarity 100.0%; Score 15; DB 2; Length 20;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 14:04:29 ; Search time 10 Seconds
(without alignments)
12.443 Million cell updates/sec

Title: GUCKER-1
Perfect score: 15
Sequence: 1 kga 3

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 3
Maximum DB seq length: 20

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	100.0	14	CAL1_CALGI	P20728 calotropis
2	15	100.0	19	ATPB_CANFA	P99504 canis faml1

ALIGNMENTS

RESULT 1
CAL1_CALGI STANDARD: PRT: 14 AA.
AC P20728;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE Calotropin DI (EC 3.4.22.-) (Fragment).
OS Calotropis gigantea (Madar) (Bowstring hemp).
OS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Gentianales; Apocynaceae; Asclepiadoideae;
OC Asclepiadeae; Calotropis.
OX NCBI_TaxID=4066;
RN [1]
RP SEQUENCE.
RA Bhattacharya D., Sengupta A., Sinha N.K.;
RT "Chemical modification and amino terminal sequence of calotropin DI
from Calotropis gigantea.";
RL Phytochemistry 26:633-636(1987).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
CC PIR: PT0026; PT0026.
DR MEROPS: C01.011; -;
DR InterPro: IPR000169; SHProt: acsite.
DR PROSITE: PS00139; THIOI_PROTEASE_CYS; PARTIAL.
DR PROSITE: PS00639; THIOI_PROTEASE_HIS; PARTIAL.

DR PROSITE: PS00640; THIOI_PROTEASE_ASN; PARTIAL.
KW Hydrolyase; Thiol protease. PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 1 1
FT NON_TER 14 14
SQ SEQUENCE 14 AA: 1715 MW: D993F0276CDA4662 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

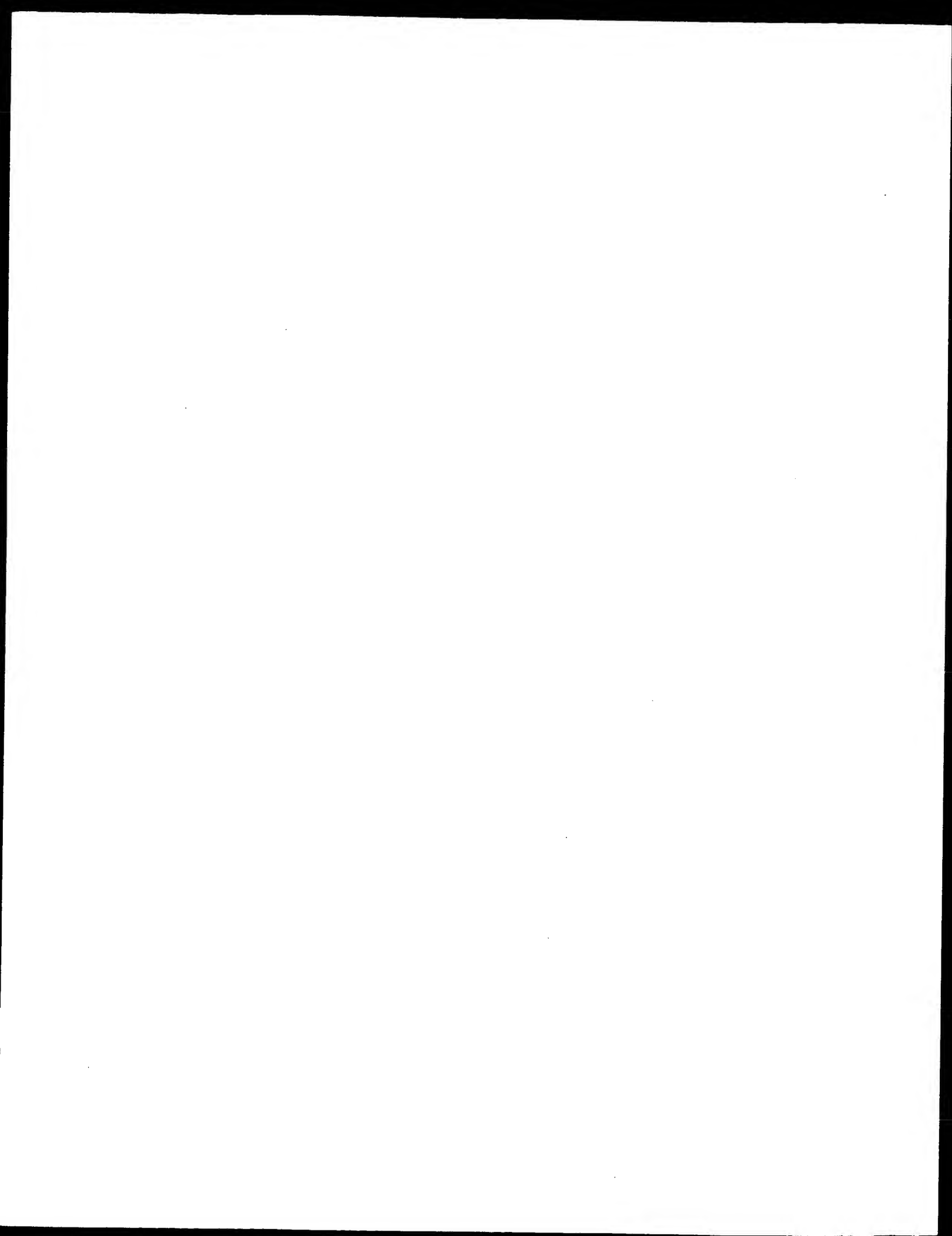
QY 1 KGA 3
Db 11 KGA 13

RESULT 2
ATPB_CANFA STANDARD: PRT: 19 AA.
ID ATPB_CANFA
AC P99504;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, last sequence update)
DT 15-JUN-2002 (Rel. 41, last annotation update)
DE ATP synthase beta chain, mitochondrial (EC 3.6.3.14) (Fragment).
GN ATP5B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
SUBUNIT.
CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
H(+) (Out).
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), Epsilon(1). CF(0)
HAS THREE MAIN SUBUNITS: A, B AND C.
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
DR HSC-2DPAGE: P99504; DOG.
DR InterPro: IPR000194; ATPase_a/bcentre.
DR PROSITE: PS00152; ATPASE_ALPHA_BETA; PARTIAL.
KW ATP synthetase; CF(1); Hydrogen ion transport; Hydrolyase; ATP-binding;
KM Mitochondrion.
FT UNSURE 8 8
FT UNSURE 17 19
FT NON_TER 19 19
SQ SEQUENCE 19 AA: 1871 MW: BB9C163FDC60BB42 CRC64;

Query Match 100.0%; Score 15; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KGA 3
Db 9 KGA 11

Search completed: November 9, 2002, 14:12:52
Job time : 10 secs



OY 1 KGA 3
111
Db 16 KGA 18

RESULT 10

S68617
histone H2A - sea urchin (Hemicentrotus pulcherrimus) (fragment)
C:Species: Hemicentrotus pulcherrimus
C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 30-Jan-1998
C:Accession: S68617
R:Onitsuki, K.; Nishikawa, Y.; Saito, H.; Munakata, H.; Kato, T.
FEBS Lett. 378, 115-120, 1996
A:Title: DNA-binding sperm proteins with oligo-arginine clusters function as potent acti
A:Reference number: S68615; PMID:96140721; PMID:8549815
A:Accession: S68617
A:Molecule type: protein
A:Residues: 1-20 <OH>
A:Experimental source: spermatozoa

Query Match 100.0%; Score 15; DB 2; Length 20;
Best local Similarity 100.0%; Pred. NO. 5.2e+02;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KGA 3
111
Db 5 KGA 7

Search completed: November 9, 2002, 14:14:09
Job time : 16 secs

QY 1 CKGATC 6
I I I I I
Db 133 CLGATC 138

RESULT 13

US-09-372-422A-12
; Sequence 12, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-12

Query Match 81.1%; Score 30; DB 4; Length 288;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGATC 6
I I I I I
Db 137 CLGATC 142

RESULT 14

US-09-372-422A-18
; Sequence 18, Application US/09372422A
; Patent No. 6313375
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-18

Query Match 81.1%; Score 30; DB 4; Length 288;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGATC 6
I I I I I
Db 142 CLGATC 147

RESULT 15

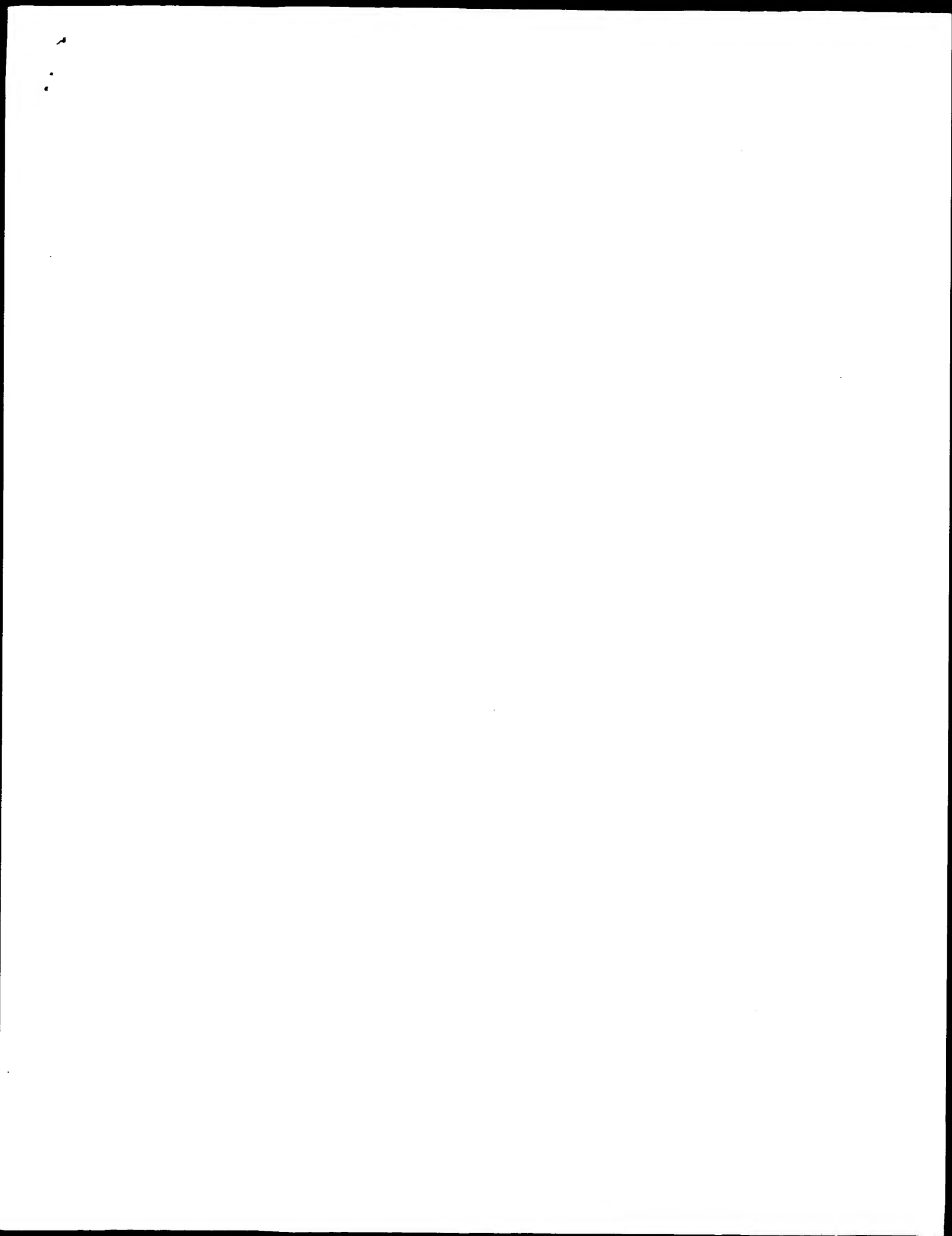
US-09-372-448A-2
; Sequence 2, Application US/09372448A
; Patent No. 6313376
; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Chaumont
; APPLICANT: Maarten Chrispeels

; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 1172
; CURRENT APPLICATION NUMBER: US/09/372,448A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/096,627
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-448A-2

Query Match 81.1%; Score 30; DB 4; Length 288;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGATC 6
I I I I I
Db 143 CLGATC 148

Search completed: November 9, 2002, 14:04:25
Job time : 9.84615 secs



; FILING DATE: 21-MAY-1992
; APPLICATION NUMBER: PCT/US93/03921
; FILING DATE: 30-APRIL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Zielinski, Bryan
; REGISTRATION NUMBER: 34,462
; REFERENCE/DOCKET NUMBER: PC8175A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 573-4585
; TELEFAX: (212) 573-1939
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 73 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: No
; ANTI-SENSE: No
; ORIGINAL SOURCE:
; ORGANISM: Filistata hibernalis
; TISSUE TYPE: venom
US-08-379-538-7

Query Match 81.1%; Score 30; DB 1; Length 73;
Best Local Similarity 83.3%; Pred. No. 75;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
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Db 21 CKGARC 26

RESULT 9
US-09-372-422A-6
; Sequence 6, Application US/09372422A
; Patent No. 6313375

; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 125
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-6

Query Match 81.1%; Score 30; DB 4; Length 125;
Best Local Similarity 83.3%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
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Db 68 CLGAIC 73

RESULT 10
US-09-053-702-2
; Sequence 2, Application US/09053702
; Patent No. 6229069

; GENERAL INFORMATION:
; APPLICANT: YAMADA, Shigehiro
; TITLE OF INVENTION: METHOD FOR CONTROLLING WATER CONTENT OF PLANT
; FILE REFERENCE: 230-122P
; CURRENT APPLICATION NUMBER: US/09/053,702
; CURRENT FILING DATE: 1998-04-02

; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 281
; TYPE: PRT
; ORGANISM: Mesembryanthemum crystallinum
US-09-053-702-2

Query Match 81.1%; Score 30; DB 4; Length 281;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| | | | |
Db 138 CLGAIC 143

RESULT 11
US-09-372-422A-8
; Sequence 8, Application US/09372422A
; Patent No. 6313375

; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Barrieu
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 0919
; CURRENT APPLICATION NUMBER: US/09/372,422A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/098,692
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-422A-8

Query Match 81.1%; Score 30; DB 4; Length 282;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| | | | |
Db 138 CLGAIC 143

RESULT 12
US-09-372-448A-4
; Sequence 4, Application US/09372448A
; Patent No. 6313376

; GENERAL INFORMATION:
; APPLICANT: Rudolf Jung
; APPLICANT: Francois Chaumont
; APPLICANT: Maarten Chrispeels
; TITLE OF INVENTION: Maize Aquaporins and Uses Thereof
; FILE REFERENCE: 1172
; CURRENT APPLICATION NUMBER: US/09/372,448A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: US 60/096,627
; PRIOR FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Zea mays
US-09-372-448A-4

Query Match 81.1%; Score 30; DB 4; Length 284;
Best Local Similarity 83.3%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,243
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 734 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-243-8

Query Match 83.8%; Score 31; DB 2; Length 734;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| ||| |
Db 330 CSGAVC 335

RESULT 6
PCT-US95-07295-8
; Sequence 8, Application PC/TUS9507295
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/07295
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: APOLLINA, MARY A
; REGISTRATION NUMBER: 34,087
; REFERENCE/DOCKET NUMBER: 19244Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908)594-3462
; TELEFAX: (908)594-4720
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 734 amino acids
; TYPE: amino acid

; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-07295-8

Query Match 83.8%; Score 31; DB 5; Length 734;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| ||| |
Db 330 CSGAVC 335

RESULT 7
US-09-193-562D-30
; Sequence 30, Application US/09193562D
; Patent No. 6309857
; GENERAL INFORMATION:
; APPLICANT: Pauli, Benedicht U.
; TITLE OF INVENTION: Nucleotide Sequences Encoding Mammalian Calcium
; TITLE OF INVENTION: Activated Chloride Channel-Adhesion Molecules
; FILE REFERENCE: 18617.0052
; CURRENT APPLICATION NUMBER: US/09/193,562D
; CURRENT FILING DATE: 1998-11-17
; PRIOR APPLICATION NUMBER: US/60/065,922
; PRIOR FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 30
; LENGTH: 1000
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-562D-30

Query Match 83.8%; Score 31; DB 4; Length 1000;
Best Local Similarity 83.3%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| ||| |
Db 200 CKGASC 205

RESULT 8
US-08-379-538-7
; Sequence 7, Application US/08379538
; Patent No. 5804554
; GENERAL INFORMATION:
; APPLICANT: Volkman, Robert A.
; APPLICANT: Saccamano, Nicholas A.
; APPLICANT: Nason II, Deane M.
; APPLICANT: Heck, Steven D.
; APPLICANT: Ronau, Robert T.
; TITLE OF INVENTION: CALCIUM CHANNEL BLOCKING POLYPEPTIDES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pfizer Inc
; STREET: 235 East 42nd Street
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/379,538
; FILING DATE: 3-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/887073

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/264,101
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-264-101-2

Query Match 83.8%; Score 31; DB 1; Length 651;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

QY 1 CKGAIC 6
| ||:|
Db 247 CSGAVC 252

RESULT 3
US-08-765-243-2
Sequence 2, Application US/08/765243
Patent No. 5935578
GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/765,243
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-765-243-2

Query Match 83.8%; Score 31; DB 1; Length 651;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

QY 1 CKGAIC 6
| ||:|
Db 247 CSGAVC 252

Query Match 83.8%; Score 31; DB 2; Length 651;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

QY 1 CKGAIC 6
| ||:|
Db 247 CSGAVC 252

RESULT 4
PCT-US95-07295-2
Sequence 2, Application PC/TUS9507295
GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
CITY: RAHWAY
STATE: NJ
COUNTRY: USA
ZIP: 07065
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/07295
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: APPOLLINA, MARY A.
REGISTRATION NUMBER: 34,087
REFERENCE/DOCKET NUMBER: 19244Y
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3462
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-07295-2

Query Match 83.8%; Score 31; DB 5; Length 651;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

QY 1 CKGAIC 6
| ||:|
Db 247 CSGAVC 252

RESULT 5
US-08-765-243-8
Sequence 8, Application US/08/765243
Patent No. 5935578
GENERAL INFORMATION:
APPLICANT: ALVES, KENNETH
APPLICANT: GUPTA, SUNIL K.
APPLICANT: HOLLIS, GREGORY F.
TITLE OF INVENTION: CONTRACEPTIVE VACCINE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: MARY A. APPOLLINA
STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:59 ; Search time 7.84615 Seconds
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Title: US-09-632-748-10

Perfect score: 37
Sequence: 1 CKGAIC 6

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2.6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	32	86.5	448	4	US-09-461-474-8
2	31	83.8	651	1	US-08-264-101-2
3	31	83.8	651	2	US-08-765-243-2
4	31	83.8	651	5	PCT-US95-07295-2
5	31	83.8	734	2	US-08-765-243-8
6	31	83.8	734	5	PCT-US95-07295-8
7	31	83.8	1000	4	US-09-193-562D-30
8	30	81.1	73	1	US-08-379-538-7
9	30	81.1	125	4	US-09-372-422A-6
10	30	81.1	281	4	US-09-053-702-2
11	30	81.1	282	4	US-09-372-422A-8
12	30	81.1	284	4	US-09-372-448A-4
13	30	81.1	288	4	US-09-372-422A-12
14	30	81.1	288	4	US-09-372-422A-18
15	30	81.1	288	4	US-09-372-448A-2
16	30	81.1	289	4	US-09-372-422A-2
17	30	81.1	289	4	US-09-372-422A-14
18	30	81.1	292	4	US-09-372-422A-4
19	29	78.4	162	2	US-08-937-931-10
20	29	78.4	162	4	US-09-285-502-10
21	29	78.4	162	4	US-09-709-126-10
22	29	78.4	162	4	US-09-871-385A-10
23	29	78.4	292	4	US-09-372-422A-10
24	29	78.4	296	4	US-09-372-422A-20
25	29	78.4	316	4	US-09-178-869-4
26	29	78.4	331	4	US-09-178-869-2
27	29	78.4	474	4	US-09-461-474-10

28	78.4	478	3	US-08-487-550-8	Sequence 8, Appli
29	78.4	760	1	US-08-547-197-2	Sequence 2, Appli
30	78.4	760	4	US-08-957-940-2	Sequence 2, Appli
31	75.7	10	4	US-09-163-095-4	Sequence 4, Appli
32	75.7	17	2	US-08-752-852A-142	Sequence 142, App
33	75.7	59	6	5466783-6	Patent No. 5466783
34	75.7	245	4	US-08-469-260A-38	Sequence 38, Appli
35	75.7	327	4	US-09-134-001C-3471	Sequence 3471, Ap
36	75.7	383	4	US-09-059-769-12	Sequence 12, Appli
37	75.7	383	4	US-09-161-94A-16	Sequence 16, Appli
38	75.7	386	4	US-09-741-154-4	Sequence 4, Appli
39	75.7	415	4	US-09-741-154-2	Sequence 2, Appli
40	75.7	466	2	US-08-604-989A-4	Sequence 4, Appli
41	75.7	491	4	US-09-030-335-2	Sequence 2, Appli
42	75.7	507	2	US-08-604-989A-5	Sequence 5, Appli
43	75.7	507	4	US-08-426-509A-2	Sequence 2, Appli
44	75.7	507	5	PCT-US95-05008-2	Sequence 2, Appli
45	75.7	527	4	US-09-311-924-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-461-474-8
; Sequence 8, Application US/09461474
; Patent No. 6278042
; GENERAL INFORMATION:
; APPLICANT: Allen, Steve
; APPLICANT: Rafalski, Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Plant Metal Transporters
; FILE REFERENCE: BBI303 US NA
; CURRENT APPLICATION NUMBER: US/09/461.474
; EARLIER FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: 60/112.562
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 8
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Zea mays
US-09-461-474-8

Query Match 86.5%; Score 32; DB 4; Length 448;
Best Local Similarity 83.3%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 CKGAIC 6
Db 65 CKGAIC 70

RESULT 2
US-08-264-101-2
; Sequence 2, Application US/08264101
; Patent No. 5693496
; GENERAL INFORMATION:
; APPLICANT: ALVES, KENNETH
; APPLICANT: GUPTA, SUNIL K.
; APPLICANT: HOLLIS, GREGORY F.
; TITLE OF INVENTION: CONTRACEPTIVE VACCINE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MARY A. APPOLLINA
; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
; CITY: RAHWAY
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk


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; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 08/881,227
; PRIOR FILING DATE: 1997-06-24
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 214
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Helicobacter pylori
; US-09-895-913A-214

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Query Match          75.7%; Score 28; DB 9; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 KGAIC 6
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Db      26 KGAIC 30

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RESULT 14
US-09-815-242-5784
; Sequence 5784, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:

```

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; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

```

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; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A

```

```

; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5784
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-5784

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Query Match          75.7%; Score 28; DB 10; Length 318;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1 CKGAIC 6
        | | | |
Db      197 CSGVIC 202

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RESULT 15
US-09-815-242-12780
; Sequence 12780, Application US/09815242
; Patent No. US20020061569A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12780
; LENGTH: 335
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-09-815-242-12780

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Query Match          75.7%; Score 28; DB 10; Length 335;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

QY      1 CKGAIC 6
        | | | |
Db      197 CSGVIC 202

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Search completed: November 9, 2002, 14:11:56
Job time : 4.69231 secs

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QY 1 CKGAIC 6
Db 75 CQGVVC 80

RESULT 10
US-09-881-752A-298
; Sequence 298, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020115078A1 Helicobacter Polypeptides in the
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 298
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-298

Query Match 75.7%; Score 28; DB 10; Length 138;
Best Local Similarity 66.7%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 14 CLGALC 19

RESULT 11
US-09-764-846-141
; Sequence 141, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ12
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 141
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-141

Query Match 75.7%; Score 28; DB 10; Length 148;
Best Local Similarity 50.0%; Pred. No. 90;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 87 CQGVVC 92

RESULT 12
US-09-895-913A-214
; Sequence 214, Application US/09895913A
; Patent No. US20020160458A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160458A1 Helicobacter Polypeptides in t
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
```

```
US-08-424-550B-38
; Sequence 38, Application US/08424550B
; Patent No. US20020119447A1
; GENERAL INFORMATION:
; APPLICANT: JOHN N. SIMONS
; APPLICANT: TAMI J. PILOT-MATIAS
; APPLICANT: GEORGE J. DAWSON
; APPLICANT: GEORGE G. SCHLAUDER
; APPLICANT: SURESH M. DESAI
; APPLICANT: THOMAS P. LEARY
; APPLICANT: ANTHONY SCOTT MUEHROFF
; APPLICANT: JAMES C. ERKER
; APPLICANT: SHERI L. BUIJK
; APPLICANT: ISA K. MUSHAWAR
; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
; NUMBER OF SEQUENCES: 716
; CORRESPONDENCE ADDRESS:
; ADDRESS: ABBOTT LABORATORIES D377/AP6D
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/424,550B
; FILING DATE:
; CLASSIFICATION: 435435
; ATTORNEY/AGENT INFORMATION:
; NAME: POREMSKI, PRISCILLA E.
; REGISTRATION NUMBER: 33,207
; REFERENCE/DOCKET NUMBER: 5527.PC.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 708-937-6365
; TELEFAX: 708-938-2623
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 245 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-424-550B-38

Query Match 75.7%; Score 28; DB 8; Length 245;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 230 CKPAVC 235

RESULT 13
US-09-895-913A-214
; Sequence 214, Application US/09895913A
; Patent No. US20020160458A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides
; TITLE OF INVENTION: Encoding No. US20020160458A1 Helicobacter Polypeptides in t
; TITLE OF INVENTION: Genome
; FILE REFERENCE: 06132/043002
; CURRENT APPLICATION NUMBER: US/09/895,913A
```

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; FILE REFERENCE: 15966-697 CIP
; CURRENT APPLICATION NUMBER: US/09/808,602
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 09/800,198
; PRIOR FILING DATE: 2001-03-05
; PRIOR APPLICATION NUMBER: 60/186,596
; PRIOR FILING DATE: 2000-03-03
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 109
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-808-602-109

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Query Match 78.4%; Score 29; DB 9; Length 188;
Best Local Similarity 66.7%; Pred. No. 74;
Matches 4; Conservative 1; Mismatches 1; Indels

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RESULT 6
US-09-950-313-6
; Sequence 6, Application US/09950313
; Patent No. US20020102610A1
; GENERAL INFORMATION:
; APPLICANT: TOWNSEND, ROBERT
; APPLICANT: ROBINSON, ANDREW
; TITLE OF INVENTION: AUTOMATED IDENTIFICATION OF PEPTIDES
; FILE REFERENCE: 9195-064
; CURRENT APPLICATION NUMBER: US/09/950,313
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: UK 0022,136.6
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,273
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 760
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-950-313-6

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Query Match          78.4%; Score 29; DB 10; Length 760;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```

RESULT 7
US-09-866-898-4
; Sequence 4, Application US/09866898
; Patent No. US20020051988A1
; GENERAL INFORMATION:
; APPLICANT: Gilcrest, Barbara A.
; APPLICANT: Yaar, Mina
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AND TREATING
; TITLE OF INVENTION: ALZHEIMER'S DISEASE
; FILE REFERENCE: BU96-09A2
; CURRENT APPLICATION NUMBER: US/09/866, 898
; CURRENT FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: 09/163,095
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: PCT/US97/04966
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/625,765

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; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Cyclic peptide
US-09-866-898-4

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Query Match          75.7%; Score 28; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 8
US-09-970-108-2
; Sequence 2, Application US/09970108
; Patent No. US20020091239A1
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L.
; TITLE OF INVENTION: Human Chemokine
; FILE REFERENCE: 00-90
; CURRENT APPLICATION NUMBER: US/09/970,108
; CURRENT FILING DATE: 2001-10-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 58
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-970-108-2

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Query Match	75.7%	Score 28;	DB 10;	Length 58;
Best Local Similarity	100.0%;	Pred. No. 40;		
Matches	5;	Conservative 0;	Mismatches 0;	Indels 0;
Gaps	0;			

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RESULT 9
US-09-925-302-523
; Sequence 523, Application US/09925302
; Patent NO. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925.302
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 523
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-523

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Query Match 75.7%; Score 28; DB 10; Length 110;
Best Local Similarity 50.0%; Pred. No. 70;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Sun Nov 10 15:29:27 2002

PRIOR APPLICATION NUMBER: 60/113,281
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,282
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,283
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,284
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,285
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/113,385
PRIOR FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: 60/114,050
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 60/114,056
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 60/114,057
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 60/114,058
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 60/114,059
PRIOR FILING DATE: 1998-12-28
PRIOR APPLICATION NUMBER: 60/114,061
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 21
LENGTH: 871
TYPE: PRT
ORGANISM: Chlamydia pneumoniae
US-09-886-468-21

Query Match 81.1%; Score 30; DB 10; Length 871;
Best Local Similarity 83.3%; Pred. No. 1.9e-02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| | | | |
Db 293 CGGAC 298

RESULT 3
US-10-001-835-187
Sequence 187, Application US/10001835
Patent No. US20020160387A1
GENERAL INFORMATION:
APPLICANT: Salceda, Susana
APPLICANT: Macina, Roberto
APPLICANT: Recipon, Hervé
APPLICANT: Cafferkey, Robert
APPLICANT: Sun, Yongming
APPLICANT: Liu, Chonghua
TITLE OF INVENTION: Compositions and Methods Relating to Ovary Specific Genes and Proteins
FILE REFERENCE: DEX-0277
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/249,997
PRIOR FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: Patentin version 3.1
SEQ ID NO 187
LENGTH: 84
TYPE: PRT
ORGANISM: Homo sapien
US-10-001-835-187

Query Match 78.4%; Score 29; DB 9; Length 84;
Best Local Similarity 50.0%; Pred. No. 36;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| | | | |
Db 52 CGGVC 57

RESULT 4

US-09-871-388-10
Sequence 10, Application US/09871388
Patent No. US20020127621A1

GENERAL INFORMATION:

APPLICANT: Rubin, Gerald M.

Pan, Duojia

Rooke, Jenny

Yavari, Reza

Xu, Tian

TITLE OF INVENTION: KUZ: A No. US20020127621A1el Family of Metalloproteases

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 BUSH STREET, SUITE 3200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/871,388

FILING DATE: 31-May-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/937,931

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: OSMAN, RICHARD A

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B97-081

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 343-4341

TELEFAX: (415) 343-4342

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 162 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-09-871-388-10

Query Match 78.4%; Score 29; DB 10; Length 162;
Best Local Similarity 66.7%; Pred. No. 65;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
| | | | |
Db 93 CSGSIC 98

RESULT 5

US-09-808-602-109

Sequence 109, Application US/09808602

Patent No. US20020155115A1

GENERAL INFORMATION:

APPLICANT: Vernet, Corine A

APPLICANT: Fernandes, Elma

APPLICANT: Shinkets, Richard A

APPLICANT: Herrman, John L

APPLICANT: Majumder, Kumud

APPLICANT: Mishra, Vishnu

APPLICANT: Mezes, Peter S

APPLICANT: MacDougall, John

TITLE OF INVENTION: NO. US20020155115A1el Proteins and Nucleic Acids Encoding Same

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2002, 14:03:09 ; Search time 3.69231 Seconds
(without alignments)
23.430 Million cell updates/sec

Title: US-09-632-748-10

Perfect score: 37
Sequence: 1 CKGAIC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 92612 seqs, 14418503 residues

Total number of hits satisfying chosen parameters: 92612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published_Applications_AA:

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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	30	81.1	871	10	US-09-886-468-21
3	29	78.4	84	9	US-10-001-835-187
4	29	78.4	162	10	US-09-871-388-10
5	29	78.4	188	9	US-09-808-602-109
6	29	78.4	760	10	US-09-950-313-6
7	28	75.7	10	10	US-09-866-898-4
8	28	75.7	58	10	US-09-970-108-2
9	28	75.7	110	10	US-09-925-302-523
10	28	75.7	138	10	US-09-881-752A-298
11	28	75.7	148	10	US-09-764-846-141
12	28	75.7	245	8	US-08-424-550B-38
13	28	75.7	316	9	US-09-895-913A-214
14	28	75.7	318	10	US-09-815-242-5784
15	28	75.7	335	10	US-09-815-242-12780
16	28	75.7	335	10	US-09-815-242-13125
17	28	75.7	431	9	US-09-808-602-113
18	28	75.7	465	10	US-09-792-200B-6
19	28	75.7	500	9	US-09-808-602-108

20 28 75.7 500 9 US-09-808-602-112 Sequence 112, Appl
21 28 75.7 500 9 US-09-808-602-114 Sequence 114, Appl
22 28 75.7 500 9 US-09-978-295A-363 Sequence 363, Appl
23 28 75.7 500 12 US-10-052-586-70 Sequence 70, Appl
24 28 75.7 507 10 US-09-977-269-2 Sequence 2, Appl
25 28 75.7 748 10 US-09-871-388-4 Sequence 4, Appl
26 28 75.7 749 10 US-09-871-388-8 Sequence 8, Appl
27 28 75.7 1055 10 US-09-855-722-2 Sequence 2, Appl
28 28 75.7 1212 10 US-09-855-722-3 Sequence 3, Appl
29 28 75.7 1214 9 US-09-945-901-54 Sequence 54, Appl
30 28 75.7 1214 9 US-10-007-747-54 Sequence 54, Appl
31 28 75.7 1219 9 US-09-945-901-50 Sequence 50, Appl
32 28 75.7 1219 9 US-10-007-747-50 Sequence 50, Appl
33 28 75.7 1231 9 US-09-945-901-48 Sequence 48, Appl
34 28 75.7 1231 9 US-10-007-747-48 Sequence 48, Appl
35 28 75.7 1236 9 US-09-945-901-6 Sequence 6, Appl
36 28 75.7 1236 9 US-10-007-747-6 Sequence 6, Appl
37 28 75.7 1238 10 US-09-855-722-5 Sequence 5, Appl
38 28 75.7 1238 10 US-09-944-849-4 Sequence 4, Appl
39 28 75.7 1239 9 US-09-945-901-52 Sequence 52, Appl
40 28 75.7 1239 9 US-10-007-747-52 Sequence 52, Appl
41 28 75.7 1244 9 US-09-945-901-46 Sequence 46, Appl
42 28 75.7 1244 9 US-10-007-747-46 Sequence 46, Appl
43 28 75.7 1602 10 US-09-778-927A-59 Sequence 59, Appl
44 27 73.0 9 10 US-09-765-086-174 Sequence 174, Appl
45 27 73.0 18 10 US-09-865-943-9 Sequence 9, Appl

ALIGNMENTS

RESULT 1

US-09-815-248-12
; Sequence 12, Application US/09815248
; Patent No. US20020098540A1

; GENERAL INFORMATION:
; APPLICANT: RASTELLI, LUCA

; APPLICANT: PENNICA, DIANE

; TITLE OF INVENTION: NOVEL POLYPEPTIDES, AND NUCLEIC ACIDS ENCODING THE SAME

; FILE REFERENCE: 10716.36

; CURRENT APPLICATION NUMBER: US/09/815,248

; PRIOR FILING DATE: 2001-08-20

; PRIOR APPLICATION NUMBER: 60/191,258

; PRIOR FILING DATE: 2000-03-22

; NUMBER OF SEQ ID NOS: 38

; SOFTWARE: Patent in Ver. 2.1

; SEQ ID NO 12

; LENGTH: 99

; TYPE: PRT

; ORGANISM: Drosophila sp.

US-09-815-248-12

Query Match 86.5%; Score 32; DB 10; Length 99;

Best Local Similarity 66.7%; Pred. No. 12;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6

DB 51 CKGVC 56

RESULT 2

US-09-886-468-21

; Sequence 21, Application US/09886468

; Patent No. US20020037293A1

; GENERAL INFORMATION:

; APPLICANT: Aventis Pasteur Limited

; TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses th

; FILE REFERENCE: 77613-5

; CURRENT APPLICATION NUMBER: US/09/886,468

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/113,280

; PRIOR FILING DATE: 1998-12-23

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG-GPBPDXY
US-10-270-837-20

Query Match 83.8%; Score 31; DB 6; Length 616;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 78 CRGSIC 83

RESULT 12

US-10-270-877-20
; Sequence 20, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG-GPBPDXY
US-10-270-877-20

Query Match 83.8%; Score 31; DB 6; Length 616;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 78 CRGSIC 83

RESULT 13

US-10-270-837-18
; Sequence 18, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT APPLICATION NUMBER: US/10/270,837
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG-GPBPDNLS
US-10-270-837-18

Query Match 83.8%; Score 31; DB 6; Length 617;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 78 CRGSIC 83
|:|:|

RESULT 14
US-10-270-877-18
; Sequence 18, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 617
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: FLAG-GPBPDNLS
US-10-270-877-18

Query Match 83.8%; Score 31; DB 6; Length 617;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 78 CRGSIC 83

RESULT 15

US-10-270-837-2
; Sequence 2, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT APPLICATION NUMBER: US/10/270,837
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-270-837-2

Query Match 83.8%; Score 31; DB 6; Length 624;
Best Local Similarity 66.7%; Pred. No. 35;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 65 CRGSIC 70

Search completed: November 9, 2002, 14:11:34
Job time : 3.53846 secs

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US-10-270-837-12
; Sequence 12, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT APPLICATION NUMBER: US/10/270,837
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bovine GPBP26
US-10-270-837-12

Query Match      83.8%; Score 31; DB 6; Length 598;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 65 CRGSIC 70

RESULT 8
US-10-270-877-8
; Sequence 8, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human GPBP26
US-10-270-877-8

Query Match      83.8%; Score 31; DB 6; Length 598;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 65 CRGSIC 70

RESULT 9
US-10-270-877-10
; Sequence 10, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
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US-10-270-837-12
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Murine GPBP26
US-10-270-877-10

Query Match      83.8%; Score 31; DB 6; Length 598;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 65 CRGSIC 70

RESULT 10
US-10-270-877-12
; Sequence 12, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Bovine GPBP26
US-10-270-877-12

Query Match      83.8%; Score 31; DB 6; Length 598;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 65 CRGSIC 70

RESULT 11
US-10-270-837-20
; Sequence 20, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT APPLICATION NUMBER: US/10/270,837
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 616
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GPBPR3
US-10-270-877-16

Query Match 83.8%; Score 31; DB 6; Length 327;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 78 CRGSIC 83

RESULT 3
US-10-270-837-22
; Sequence 22, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/10/270,837
; PRIOR FILING DATE: 2002-10-11
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: FLAG-GPBPSXY/NLS
US-10-270-837-22

Query Match 83.8%; Score 31; DB 6; Length 596;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 78 CRGSIC 83

RESULT 4
US-10-270-877-22
; Sequence 22, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/10/270,877
; PRIOR FILING DATE: 2002-10-11
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: FLAG-GPBPSXY/NLS
US-10-270-877-22

Query Match 83.8%; Score 31; DB 6; Length 596;

Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 78 CRGSIC 83

RESULT 5
US-10-270-837-8
; Sequence 8, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/10/270,837
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human GPBP26
US-10-270-837-8

Query Match 83.8%; Score 31; DB 6; Length 598;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 65 CRGSIC 70

RESULT 6
US-10-270-837-10
; Sequence 10, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: US/10/270,837
; PRIOR FILING DATE: 2002-10-11
; PRIOR FILING DATE: 2000-02-24
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 598
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Murine GPBP26
US-10-270-837-10

Query Match 83.8%; Score 31; DB 6; Length 598;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
|:|:|
Db 65 CRGSIC 70

RESULT 7

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 9, 2002, 14:01:49 ; Search time 2.53846 Seconds
(without alignments)
26.619 Million cell updates/sec

Title: US-09-632-748-10

Perfect score: 37

Sequence: 1 CKGAIC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 39427 seqs, 11261862 residues

Total number of hits satisfying chosen parameters: 39427

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New.*

- 1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep.*
- 2: /cgn2_6/ptodata/2/paa/US05_NEW_COMB.pep.*
- 3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep.*
- 4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep.*
- 5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep.*
- 6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep.*
- 7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	83.8	327	6	US-10-270-837-16
2	31	83.8	327	6	US-10-270-877-16
3	31	83.8	596	6	US-10-270-837-22
4	31	83.8	596	6	US-10-270-877-22
5	31	83.8	598	6	US-10-270-837-8
6	31	83.8	598	6	US-10-270-837-10
7	31	83.8	598	6	US-10-270-837-12
8	31	83.8	598	6	US-10-270-877-8
9	31	83.8	598	6	US-10-270-877-10
10	31	83.8	598	6	US-10-270-877-12
11	31	83.8	616	6	US-10-270-837-20
12	31	83.8	616	6	US-10-270-877-20
13	31	83.8	617	6	US-10-270-837-18
14	31	83.8	617	6	US-10-270-877-18
15	31	83.8	624	6	US-10-270-837-2
16	31	83.8	624	6	US-10-270-837-4
17	31	83.8	624	6	US-10-270-837-6
18	31	83.8	624	6	US-10-270-877-2
19	31	83.8	624	6	US-10-270-877-4
20	31	83.8	624	6	US-10-270-877-6
21	31	83.8	637	6	US-10-270-837-24
22	31	83.8	637	6	US-10-270-877-24
23	29	78.4	110	6	US-10-264-237-2278
24	29	78.4	497	6	US-10-230-437-56
25	28	75.7	170	5	US-09-513-999C-5046
26	28	75.7	170	5	US-09-513-999C-5047

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27 75.7 327 6 US-10-092-411A-3471 Sequence 3471, Ap
28 75.7 500 6 US-10-145-087A-363 Sequence 363, App
29 75.7 500 6 US-10-143-031A-363 Sequence 363, App
30 75.7 500 6 US-10-145-092A-363 Sequence 363, App
31 75.7 500 6 US-10-162-522A-363 Sequence 363, App
32 75.7 500 6 US-10-165-038A-363 Sequence 363, App
33 75.7 500 6 US-10-170-481A-363 Sequence 363, App
34 75.7 500 6 US-10-170-481A-363 Sequence 363, App
35 75.7 500 6 US-10-172-039A-363 Sequence 363, App
36 75.7 500 6 US-10-145-010A-363 Sequence 363, App
37 75.7 500 6 US-10-145-088A-363 Sequence 363, App
38 75.7 500 6 US-10-145-129A-363 Sequence 363, App
39 75.7 500 6 US-10-125-923A-70 Sequence 70, Appl
40 75.7 500 6 US-10-165-353A-363 Sequence 363, App
41 75.7 944 6 US-10-268-473-4 Sequence 4, Appl
42 73.0 108 6 US-10-264-237-1949 Sequence 1949, Ap
43 73.0 132 5 US-09-513-999C-6410 Sequence 6410, Ap
44 73.0 171 6 US-10-223-089-346 Sequence 346, App
45 73.0 266 6 US-10-145-087A-456 Sequence 456, App

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ALIGNMENTS

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RESULT 1
US-10-270-837-16
; Sequence 16, Application US/10270837
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD2
; CURRENT APPLICATION NUMBER: US/10/270,837
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: GPBPR3
US-10-270-837-16

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Query Match      83.8%   Score 31; DB 6; Length 327;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGAIC 6
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Db 78 CRGSIC 83

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RESULT 2
US-10-270-877-16
; Sequence 16, Application US/10270877
; GENERAL INFORMATION:
; APPLICANT: Saus, Juan
; TITLE OF INVENTION: Goodpasture Binding Protein
; FILE REFERENCE: 98-723-AD1
; CURRENT APPLICATION NUMBER: US/10/270,877
; CURRENT FILING DATE: 2002-10-11
; PRIOR APPLICATION NUMBER: 09/512,563
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/121,483
; PRIOR FILING DATE: 1999-02-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 16
; LENGTH: 327

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A:Reference number: Z18456
 A:Accession: T16073
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-975 <GEI>
 A:Cross-references: EMBL:U28737; NID:g860717; PID:g860722; PIDN:AAA68275.1; CESP:FL4B8.5
 A:Experimental source: strain Bristol N2
 C:Genetics:
 A:Gene: CESP:FL4B8.5
 A:Introns: 48/2; 84/2; 114/1; 191/2; 227/3; 291/2; 308/2; 325/3; 350/3; 383/2; 416/2; 48

Query Match 83.8%; Score 31; DB 2; Length 975;
 Best Local Similarity 86.7%; Pred. No. 2.3e+02;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
 |||||
 DB 740 CKGVLC 745

RESULT 13
 B86483
 protein F5J5.15 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 A:Accession: B86483
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 ansen, N.F.; Hughes, B.; Huizar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: B86483
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1617 <STO>
 A:Cross-references: GB:AE005172; NID:g6598587; PIDN:AAF18642.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F5J5.15
 A:Map position: 1

Query Match 83.8%; Score 31; DB 2; Length 1617;
 Best Local Similarity 83.3%; Pred. No. 3.5e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
 |||||
 DB 1549 CKGDIC 1554

RESULT 14
 S65712
 metallothionein 1 - rat (fragments)
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-May-1997
 A:Accession: S65712
 R:Salto, S.; Hunziker, P.E.
 Biochim. Biophys. Acta 1289, 65-70, 1996
 A:Title: Differential sensitivity of metallothionein-1 and -2 in liver of zinc-injected
 A:Reference number: S65712; MUID:96195842; PMID:8605234
 A:Accession: S65712
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-23;24-46;47-52 <SAI>
 C:Superfamily: metallothionein
 C:Keywords: blocked amino end

Query Match 81.1%; Score 30; DB 2; Length 52;

Best Local Similarity 83.3%; Pred. No. 36;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
 |||||
 DB 43 CKGAKC 48

RESULT 15
 H64324
 ferredoxin 2[4Fe-4S] - Methanococcus jannaschii
 C:Species: Methanococcus jannaschii
 C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
 A:Accession: H64324
 R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
 zson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
 Science 273, 1058-1073, 1996
 A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
 A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
 A:Reference number: A64300; MUID:96337999; PMID:8688087
 A:Accession: H64324
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-65 <BUL>
 C:Genetics:
 A:Cross-references: GB:U67476; GB:L77117; NID:g1590942; PIDN:AAB98183.1; PID:g1590944
 A:Map position: FOR192376-192573
 A:Start codon: GTG
 C:Superfamily: ferredoxin 2[4Fe-4S]; ferredoxin 2[4Fe-4S] homology
 C:Keywords: 4Fe-4S; electron transfer; iron-sulfur protein; metalloprotein
 F:6-63/Domain: ferredoxin 2[4Fe-4S] homology <FFR>
 F:13,18,21,55/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted
 F:25,45,48,51/Binding site: 4Fe-4S cluster (Cys) (covalent) #status predicted

Query Match 81.1%; Score 30; DB 2; Length 65;
 Best Local Similarity 83.3%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
 |||||
 DB 13 CKGAEC 18

Search completed: November 9, 2002, 14:03:44
 Job time : 9.30769 secs

A:Gene: APE2344
C:Superfamily: lipolic acid synthase

Query Match 83.8%; Score 31; DB 2; Length 295;
Best Local Similarity 66.7%; Pred. No. 90;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGAIC 6
|:|:|:|

Db 34 CEGALC 39

RESULT 8

D86357 alcohol dehydrogenase (EC 1.-.-.-) [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Aug-2002

C:Accession: D86357

R:Theologas, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
ansen, N.F.; Hughes, B.; Huizar, L.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86357

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-388 <STO>

A:Cross-references: GB:AE005172; NID:G6587845; PIDN:AAF18534.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C:Keywords: oxidoreductase; zinc

F:53,76,185/Binding site: zinc, catalytic (Cys, His, Cys) #status predicted

Query Match 83.8%; Score 31; DB 2; Length 388;

Best Local Similarity 83.3%; Pred. No. 1.1e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGAIC 6

|:|:|:|

Db 16 CKAAC 21

RESULT 9

T51805

nodulin-like protein [Imported] - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C:Accession: T51805

R:Szczyglowski, K.; Kapranov, P.; Hamburger, D.; de Bruijn, F.J.

Plant Mol. Biol. 37, 651-661, 1998

A:Title: The Lotus Japonicus LjNOD70 nodulin gene encodes a protein with similarities to

A:Reference number: Z25457

A:Accession: T51805

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-559 <SZC>

A:Cross-references: EMBL:AF031244; PIDN:AAC39501.1

C:Function:

A:Description: associated with late stages in Lotus japonicus nodule development and/or

Query Match 83.8%; Score 31; DB 2; Length 559;

Best Local Similarity 66.7%; Pred. No. 1.5e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGAIC 6

|:|:|:|

Db 16 CKAAC 21

Db 540 CRGSIC 545

RESULT 10

JC4861

fertilin beta chain - human

C:Species: Homo sapiens (man)

C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 21-Jan-2000

C:Accession: JC4861

R:Gupta, S.K.; Alves, K.; O'Neill Palladino, L.; Mark, G.E.; Hollis, G.F.

Biochem. Biophys. Res. Commun. 224, 318-326, 1996

A:Title: Molecular cloning of the human fertilin beta subunit.

A:Reference number: JC4861; MUID:96295488; PMID:8702389

A:Accession: JC4861

A:Molecule type: mRNA

A:Residues: 1-734 <GUP>

A:Cross-references: GB:U38805; NID:G4151118; PIDN:AA04206.1; PID:G4151119

C:Comment: This protein is an integral sperm membrane glycoprotein, and plays a role

C:Superfamily: mouse meltrin alpha; disintegrin homology

C:Keywords: glycoprotein; integrin binding; transmembrane protein

F:382-734/Product: fertilin beta chain #status predicted <NAV>

F:382-734/Domain: disintegrin homology <DIS>

F:448-450/Region: integrin binding #status predicted

F:686-708/Domain: transmembrane #status predicted <TMM>

F:121,219,352,458,565/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 83.8%; Score 31; DB 2; Length 734;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CKGAIC 6

|:|:|:|

Db 330 CSGAVC 335

RESULT 11

T18649

hypothetical protein B0024.14 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T18649

R:McMurray, A.

submitted to the EMBL Data Library, April 1996

A:Reference number: Z19001

A:Accession: T18649

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-884 <WIL>

A:Cross-references: EMBL:Z71178; PIDN:CAA94886.1; GSPDB:GN00023; CESP:B0024.14

A:Experimental source: clone B0024

C:Genetics:

A:Gene: CESP:B0024.14

A:Map position: 5

A:Introns: 46/3; 84/1; 212/1; 307/2; 345/2; 394/1; 424/2; 481/1; 596/1; 702/1; 765/3;

Query Match 83.8%; Score 31; DB 2; Length 884;

Best Local Similarity 66.7%; Pred. No. 2.2e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CKGAIC 6

|:|:|:|

Db 127 CRGSIC 132

RESULT 12

T16073

hypothetical protein F14B8.5 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16073

R:Geisel, C.

submitted to the EMBL Data Library, June 1995

A:Description: The sequence of C. elegans cosmid F14B8.

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 187 CEGAVC 192

RESULT 3

C64890
probable electron transfer protein - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C:Accession: C64890
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shaoh, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: C64890
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-356 <BLAT>
A:Cross-references: GB:AE000236; GB:U00096; NID:gl787652; PIDN:AACT4474.1; PID:gl787658;
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: phthalate dioxygenase reductase; cytochrome-b5 reductase homology; ferredoxin
E:Keywords: 2Fe-2S; electron transfer; iron-sulfur protein; metalloprotein; transmembrane
E:116-132/Domain: transmembrane #status predicted <TM01>
E:284-338/Domain: ferredoxin [2Fe-2S] homology <FER>
E:299,304,307,337/Binding site: 2Fe-2S cluster (Cys) (covalent) #status predicted

Query Match 86.5%; Score 32; DB 2; Length 356;

Best Local Similarity 66.7%; Pred. No. 67;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 299 CKGGVC 304

RESULT 4

VGVNVJ
spike glycoprotein G precursor - vesicular stomatitis New Jersey virus
C:Species: vesicular stomatitis New Jersey virus
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A04118
R:Gallione, C.J.; Rose, J.K.
J. Virol. 46, 162-169, 1983
A:Title: Nucleotide sequence of a cDNA clone encoding the entire glycoprotein from the New Jersey virus
A:Reference number: A04118; MUID:83138980; PMID:6298453
A:Accession: A04118
A:Molecule type: mRNA
A:Residues: 1-517 <GAL>
A:Cross-references: GB:V01214; NID:g61839; PIDN:CAA24525.1; PID:g61840
C:Genetics:
A:Gene: G
C:Superfamily: rhabdovirus spike glycoprotein G
C:Keywords: glycoprotein; spike protein; transmembrane protein
E:1-22/Domain: signal sequence #status predicted <SIG>
E:23-517/Product: spike glycoprotein G #status predicted <SGG>
E:473-489/Domain: transmembrane #status predicted <TM>
E:179,340/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 86.5%; Score 32; DB 1; Length 517;

Best Local Similarity 83.3%; Pred. No. 90;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 169 CKGQIC 174

RESULT 5

H81730
probable lipoic acid synthetase APE2344 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: E72462
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
pyrum pernix strain K1
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72462
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <KAW>
A:Cross-references: DDBJ:AF000064; NID:g5105945; PIDN:BAA81357.1; PID:g5106046
A:Experimental source: strain K1
C:Genetics:

ribosomal protein L32 TC0195 [imported] - Chlamydia muridarum (strain Nigg)
C:Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000
C:Accession: H81730
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hicke
r, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzbe
rger, E.; et al. Nucleic Acids Res. 28, 1397-1406, 2000
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39
A:Reference number: A81500; MUID:20150255; PMID:10684935
A:Accession: H81730
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-59 <TET>
A:Cross-references: GB:AE002286; GB:AE002160; NID:g7190225; PIDN:AAF39069.1; PID:g719
A:Experimental source: strain Nigg (MoPn)
C:Genetics:
A:Gene: TC0195
C:Superfamily: Escherichia coli ribosomal protein L32

Query Match 83.8%; Score 31; DB 2; Length 59;

Best Local Similarity 66.7%; Pred. No. 25;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 25 CSGAVC 30

RESULT 6

T14600
plasma membrane major intrinsic protein 2 - beet
N:Alternate names: probable aquaporin
C:Species: Beta vulgaris (beet)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999
C:Accession: T14600
R:Qi, X.; Mu, H.; Wasserman, B.P.
submitted to the EMBL Data Library, June 1996
A:Reference number: Z18157
A:Accession: T14600
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-281 <Q1>
A:Cross-references: EMBL:U60148; NID:gl402834; PID:gl402835
A:Experimental source: strain Detroit dark red
C:Superfamily: lens fiber membrane major intrinsic protein

Query Match 83.8%; Score 31; DB 2; Length 281;

Best Local Similarity 83.3%; Pred. No. 87;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 127 CAGAIC 132

RESULT 7

E72462
probable lipoic acid synthetase APE2344 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: E72462
R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Ta
awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.
DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero
pyrum pernix strain K1
A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: E72462
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-295 <KAW>
A:Cross-references: DDBJ:AF000064; NID:g5105945; PIDN:BAA81357.1; PID:g5106046
A:Experimental source: strain K1
C:Genetics:

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:34 ; Search time 8.30769 Seconds
(without alignments)
69.430 Million cell updates/sec

Title: US-09-632-748-10

Perfect score: 37

Sequence: 1 CKGAIC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	89.2	626	2 S52209	noncapsid protein
2	32	86.5	245	2 A13485	hypothetical prote
3	32	86.5	356	2 C64890	probable electron
4	32	86.5	517	1 VGVNVJ	spike glycoprotein
5	31	83.8	59	2 H81730	ribosomal protein
6	31	83.8	281	2 T14600	plasma membrane ma
7	31	83.8	295	2 E72462	probable lipoid ac
8	31	83.8	388	2 D86357	alcohol dehydrogen
9	31	83.8	559	2 T51805	nodulin-like prote
10	31	83.8	734	2 JC4861	fertilin beta cha
11	31	83.8	884	2 T18649	hypothetical prote
12	31	83.8	975	2 T16073	hypothetical prote
13	31	83.8	1617	2 B86483	protein F535.15 [1
14	30	81.1	52	2 S65712	metallothionein 1
15	30	81.1	65	2 H64324	ferredoxin 2[4Fe-4
16	30	81.1	124	2 AG3252	hypothetical cytos
17	30	81.1	130	2 F72120	probable ferredoxi
18	30	81.1	130	2 D86501	ferredoxin [import
19	30	81.1	187	2 T09817	probable water cha
20	30	81.1	198	2 T09796	drought-induced ma
21	30	81.1	216	2 T04368	plasma membrane in
22	30	81.1	278	2 A84545	hypothetical prote
23	30	81.1	280	2 T05780	plasma membrane in
24	30	81.1	281	2 T09124	probable aquaporin
25	30	81.1	283	2 T12434	probable plasma me
26	30	81.1	284	2 T12557	m1pE protein - com
27	30	81.1	284	2 T03794	aquaporin NT2 - co
28	30	81.1	285	2 T12342	major intrinsic pr
29	30	81.1	285	2 T12435	probable plasma me

30 30 81.1 285 2 S44085 plasma membrane in
31 30 81.1 285 2 T06434 plasma membrane in
32 30 81.1 285 2 D84789 hypothetical prote
33 30 81.1 285 2 E84789 hypothetical prote
34 30 81.1 286 2 T47935 plasma membrane in
35 30 81.1 286 2 T14601 plasma membrane ma
36 30 81.1 286 2 T04367 plasma membrane in
37 30 81.1 286 2 S42542 ripening-associate
38 30 81.1 286 2 T02451 plasma membrane in
39 30 81.1 286 2 T06738 probable plasma me
40 30 81.1 286 2 A86147 hypothetical prote
41 30 81.1 287 2 T09791 drought-induced ma
42 30 81.1 287 2 T12440 m1pC protein - com
43 30 81.1 287 2 T05378 probable plasma me
44 30 81.1 287 2 S44084 plasma membrane in
45 30 81.1 287 2 S60455 transmembrane prot

ALIGNMENTS

RESULT 1

S52209

noncapsid protein NS1 - muscovy duck parvovirus

N;Alternate names: nonstructural protein NS1; NS1 protein

C;Species: muscovy duck parvovirus

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C;Accession: S52209

R;Zadoni, Z.; Erdei, J.; Nagy, J.; Kisari, J.

submitted to the EMBL Data Library, September 1993

A;Reference number: S52209

A;Accession: S52209

A;Molecule type: DNA

A;Residues: 1-626 <ZAD>

A;Cross-references: EMBL:X75093; NID:g609091; PIDN:CAA52983.1; PID:g609092

A;Experimental source: strain FM

C;Genetics:

A;Gene: NS1

C;Superfamily: parvovirus noncapsid protein

C;Keywords: noncapsid protein

Query Match 89.2%; Score 33; DB 2; Length 626;
Best Local Similarity 66.7%; Pred. No. 67;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6

|||:|

Db 406 CKGSVC 411

RESULT 2

A13485

hypothetical protein BMEI1871 [imported] - Brucella melitensis (strain 16M)

C;Species: Brucella melitensis

C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C;Accession: A13485

R;DelVecchio, V.G.; Kapratl, V.; Redkar, R.J.; Patra, G.; Mufier, C.; Los, T.; Ivanov

; Mazur, M.; Goldsman, E.; Selkov, E.; Elizer, P.H.; Hagius, S.; O'Callaghan, D.; Let

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A;Title: The genome sequence of the facultative intracellular pathogen Brucella melit

A;Reference number: AD3252; PMID:11756688

A;Accession: A13485

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-245 <KUR>

A;Cross-references: GB:AE008917; PIDN:AAL53052.1; PID:g17983912; GSPDB:GN00190

A;Experimental source: strain 16M

C;Genetics:

A;Gene: BMEI1871

A;Map position: I

Query Match 86.5%; Score 32; DB 2; Length 245;
Best Local Similarity 66.7%; Pred. No. 50;

KW Transport; Transmembrane: Multigene family.
SQ SEQUENCE 285 AA; 30429 MW; D51213A68EEBB508 CRC64;
Query Match 81.1%; Score 30; DB 1; Length 285;
Best Local Similarity 83.3%; Pred. NO. 48;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CKGAIC 6
Db 131 CLGAIC 136

Search completed: November 9, 2002, 14:01:46
Job time : 6.61538 secs

FT CA_BIND 32 32 VIA CARBONYL OXYGEN (BY SIMILARITY).
 FT CA_BIND 49 49 BY SIMILARITY.
 SQ SEQUENCE 119 AA; 12856 MW; 229241793FA826F7 CRC64;

Query Match 81.1%; Score 30; DB 1; Length 119;
 Best Local Similarity 66.7%; Pred. No. 23;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
 DB 85 CKGFVC 90

RESULT 14

WC2C_ARATH STANDARD; PRT; 285 AA.

AC P43287; Q9SKR8;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Plasma membrane intrinsic protein 2B.
 GN PIP2B OR AT2G37170 OR T2N18.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Landsberg erecta; TISSUE=Root;

RX MEDLINE=95004661; PubMed=7920711;

RA Kammerloher W., Fischer U., Plechottka G.P., Schaeffner A.R.;

RT "Water channels in the plant plasma membrane cloned by

RT immunoselection from a mammalian expression system.";

RL Plant J. 6:187-199(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Buell L.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,

RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,

RA Venter J.C.;

RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis

RT thaliana.";

RL Nature 402:761-768(1999).

CC -!- FUNCTION: WATER CHANNEL. PROTEIN IN PLASMA MEMBRANE.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).

CC -----
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CC -----

CC EMBL; X75884; CAA53478.1; -

CC EMBL; AC006260; AAD18142.1; -

CC HSSP; P29972; IH6I.

CC InterPro; IPR000425; MIP_family.

CC Pfam; PF00230; MIP; 1.

CC PRINTS; PR00783; MINTRINSICP.

CC ProDom; PD000295; MIP_family; 1.

CC TIGRFAMs; TIGR00861; MIP; 1.

CC PROSITE; PS02221; MIP; 1.

CC Transport; Transmembrane; Multigene family.

CC KW -CONFLICT 141 143 VKA -> ROS (IN REF. 1).

FT CONFLICT 234 234 A -> S (IN REF. 1).
 SQ SEQUENCE 285 AA; 30453 MW; 04364AFE7531EE10 CRC64;

Query Match 81.1%; Score 30; DB 1; Length 285;
 Best Local Similarity 83.3%; Pred. No. 48;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
 DB 131 CLGAIC 136

RESULT 15

WC2C_ARATH STANDARD; PRT; 285 AA.

AC P30302;
 DT 01-APR-1993 (Rel. 25, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Plasma membrane intrinsic protein 2C (Water-stress induced tonoplast

DE intrinsic protein) (WSI-TIP).

GN PIP2C OR RD28 OR AT2G37180 OR T2N18.6.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.

OX NCBI_TaxID=3702;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RA Yamauchi-Shinozaki K., Koizumi M., Urao S., Shinozaki K.;

RT "Molecular cloning and characterization of 9 cDNAs for genes that are

RT responsive to desiccation in Arabidopsis thaliana: sequence analysis

RT of one cDNA clone that encodes a putative transmembrane channel

RT protein.";

RL Plant Cell Physiol. 33:217-224(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;

RX MEDLINE=20083487; PubMed=10617197;

RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

RA Buell L.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,

RA Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L.,

RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,

RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,

RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,

RA Venter J.C.;

RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis

RT thaliana.";

RL Nature 402:761-768(1999).

CC -!- FUNCTION: WATER CHANNEL. PROTEIN IN PLASMA MEMBRANE.

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- INDUCTION: BY DEHYDRATION.

CC -!- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).

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CC -----

CC EMBL; D13254; BAA02520.1; -

CC EMBL; AC006260; AAD18141.1; -

CC HSSP; P29972; IH6I.

CC InterPro; IPR000425; MIP_family.

CC Pfam; PF00230; MIP; 1.

CC PRINTS; PR00783; MINTRINSICP.

CC ProDom; PD000295; MIP_family; 1.

CC TIGRFAMs; TIGR00861; MIP; 1.

CC PROSITE; PS00221; MIP; 1.

```

FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 566 566 MISSING (IN REF. 2).
FT CONFLICT 21 21 D -> H (IN REF. 3).
FT CONFLICT 99 99 E -> D (IN REF. 3).
FT CONFLICT 106 106 V -> G (IN REF. 3).
FT CONFLICT 170 170 V -> A (IN REF. 2).
FT CONFLICT 288 288 H -> D (IN REF. 2 AND 3).
FT CONFLICT 321 321 T -> I (IN REF. 2 AND 3).
FT CONFLICT 388 388 EEC -> DEF (IN REF. 3).
FT CONFLICT 396 396 G -> S (IN REF. 3).
FT CONFLICT 501 501 G -> S (IN REF. 3).
FT CONFLICT 529 529 D -> Y (IN REF. 3).
FT CONFLICT 579 579 S -> G (IN REF. 3).
FT CONFLICT 588 588 W -> L (IN REF. 3).
FT CONFLICT 603 603 N -> D (IN REF. 3).
FT CONFLICT 629 629 NK -> KQ (IN REF. 3).
FT CONFLICT 638 638 S -> F (IN REF. 3).
SQ SEQUENCE 735 AA; 82466 MW; BBF27B8BEC7F92D3 CRC64;

Query Match 83.8%; Score 31; DB 1; Length 735;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
DB 331 CSGAVC 336

RESULT 12
FER4_METJA
ID FER4_METJA STANDARD; PRT; 62 AA.
AC Q57652;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Putative ferredoxin MJ0199.
GN MJ0199.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=868987;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
jannaschii."
RT Science 273:1058-1073(1996).
RL Science 273:1058-1073(1996).
CC -!- COFACTOR: BINDS TWO 4FE-4S CLUSTERS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE BACTERIAL TYPE FERREDOXIN FAMILY.
CC -----
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CC -----
CC EMBL; U67476; AAB98183.1; ALT_INIT.
DR HSP; P00209; IFXD.
DR TIGR; MJ0199; -.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR Pfam; PF00037; fer4; 2.

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DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW Hypothetical protein; Electron transport; Iron-sulfur; 4Fe-4S;
FT METAL 10 10 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 15 15 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 18 18 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 22 22 IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
FT METAL 42 42 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 45 45 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 48 48 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
FT METAL 52 52 IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 62 AA; 6650 MW; C46FA4A11722276A CRC64;

Query Match 81.1%; Score 30; DB 1; Length 62;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
DB 10 CKGAEC 15

RESULT 13
PA21_ACAAN STANDARD; PRT; 119 AA.
ID PA21_ACAAN
AC P81236;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Acanthin I) (Phosphatidylcholine
DE 2-acylhydrolase).
OS Acanthophis antarcticus (Common death adder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Acanthophis.
OX NCBI_TaxID=8605;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=98303724; PubMed=9637731;
RA Chow G., Subburaju S., Kini R.M.;
RT "Purification, characterization, and amino acid sequence
RT determination of acanthins, potent inhibitors of platelet aggregation
RT from Acanthophis antarcticus (common death adder) venom.";
RL Arch. Biochem. Biophys. 354:232-238(1998).
CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE 2-
CC ACYL GROUPS IN 3-SN-PHOSPHOGLYCERIDES. EXHIBITS ANTIPLATELET
CC ACTIVITY.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
DR HSP; P00609; 2NOT.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR PRODOM; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR Hydroxylase; Lipid degradation; Calcium: Venom.
KW ACT_SITE 48 48 BY SIMILARITY.
FT ACT_SITE 93 93 BY SIMILARITY.
FT DISULFID 11 71 BY SIMILARITY.
FT DISULFID 27 118 BY SIMILARITY.
FT DISULFID 29 45 BY SIMILARITY.
FT DISULFID 44 99 BY SIMILARITY.
FT DISULFID 51 92 BY SIMILARITY.
FT DISULFID 60 85 BY SIMILARITY.
FT DISULFID 78 90 BY SIMILARITY.
FT CA_BIND 28 28 VIA CARBONYL OXYGEN (BY SIMILARITY).
FT CA_BIND 30 30 VIA CARBONYL OXYGEN (BY SIMILARITY).

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CC EMBL; AF232932; AAG42048.1; -
 CC EMBL; AF232934; AAG42050.1; -
 CC EMBL; AK012989; BAB28581.1; -
 CC MGD; MGI:1915268; Col4a3bp.
 CC InterPro; IPR001849; PH.
 CC InterPro; IPR002913; START.
 CC Pfam; PF00169; PH; 1.
 CC Pfam; PF01852; START; 1.
 CC SMART; SM00233; PH; 1.
 CC SMART; SM00234; START; 1.
 CC PROSITE; PS50003; PH_DOMAIN; 1.
 CC PROSITE; PS50846; START; 1.
 CC Transferrase; Coiled coil; Alternative splicing.
 CC FT DOMAIN 23 117 PH
 CC FT DOMAIN 263 303 COILED COIL (POTENTIAL).
 CC FT DOMAIN 389 618 START.
 CC FT VARSPLIC 371 396 MISSING (IN ISOFORM 2).
 CC SQ SEQUENCE 624 AA; 71111 MW; FD708AFFB23FCD31 CRC64;

Query Match 83.8%; Score 31; DB 1; Length 624;

Best Local Similarity 66.7%; Pred. No. 60;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGATC 6

Db 65 CRGSC 70

RESULT 11

AD02_HUMAN
 ID AD02_HUMAN STANDARD; PRT; 735 AA.
 AC Q99965; P78326;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADAM 2 precursor (A disintegrin and metalloproteinase domain 2)
 DE (Fertilin beta subunit) (PH-30) (PH30).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97193554; PubMed=9041139;
 RA Vidua C.M., von Kap-Herr C., Golden W.L., Eddy R.L., Shows T.B.,
 RA Herr J.C.;
 RT "Human fertilin beta: identification, characterization, and
 RT chromosomal mapping of an ADAM gene family member.";
 RT Mol. Reprod. Dev. 46:363-369(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=96293488; PubMed=8702389;
 RA Gupta S.K., Alves K., Palladino L.O., Mark G.E., Hollis G.F.;
 RT "Molecular cloning of the human fertilin beta subunit.";
 RT Biochem. Biophys. Res. Commun. 224:318-326(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Testis;
 RX MEDLINE=97224507; PubMed=9070941;
 RA Burkin H.R., Burkin D.J., Davey P.M., Griffin D.K., Affara N.A.;
 RT "Mapping, sequence, and expression analysis of the human fertilin beta
 RT gene (FTNB).";
 RT Genomics 40:190-192(1997).
 RL

-|- FUNCTION: SPERM SURFACE MEMBRANE PROTEIN THAT MAY BE INVOLVED IN
 CC SPERM-EGG PLASMA MEMBRANE ADHESION AND FUSION DURING
 CC FERTILIZATION. COULD HAVE A DIRECT ROLE IN SPERM-ZONA BINDING OR
 CC MIGRATION OF SPERM FROM THE UTERUS INTO THE OVIDUCT. INTERACTIONS
 CC WITH EGG MEMBRANE COULD BE MEDIATED VIA BINDING BETWEEN ITS
 CC DISINTEGRIN-LIKE DOMAIN TO ONE OR MORE INTEGRINS RECEPTORS ON THE
 CC EGG. THIS IS A NON CATALYTIC METALLOPROTEASE-LIKE PROTEIN.
 CC SUBCELLULAR LOCATION: Type I membrane protein.
 CC TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN SPERMATOGENIC CELLS
 CC IN THE SEMINIFEROUS CELLS. NOT DETECTED IN FETAL TISSUES.
 CC DOMAIN: A CONSERVED TRIPEPTIDE MOTIF (FEE) WITHIN DISINTEGRIN-LIKE
 CC DOMAIN COULD BE INVOLVED IN THE BINDING TO EGG INTEGRIN RECEPTOR
 CC AND THUS COULD MEDIATE SPERM/EGG BINDING.
 CC PTM: THE SIGNAL AND THE METALLOPROTEASE DOMAIN ARE CLEAVED DURING
 CC THE EPIDIDYMAL MATURATION OF THE SPERMATOZOON.
 CC MISCELLANEOUS: IN MAMMALS, EXISTS AS A HETERODIMER COMPOSED OF AN
 CC ALPHA AND BETA SUBUNITS. IN HUMAN, FERTILIN ALPHA IS A PSEUDOGENE.
 CC SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12B.
 CC SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC SIMILARITY: CONTAINS 1 DISINTEGRIN DOMAIN.
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EMBL; U52370; AAC51110.1; -
 EMBL; U38805; AAD04206.1; -
 EMBL; X93374; CAA67753.1; -
 HSP; P17494; 1KST.
 MEROPS; M12.950; -
 Genew; HGNC:198; ADAM2.
 MIM; 601533; -
 InterPro; IPR001762; Disintegrin.
 InterPro; IPR000561; EGF-like.
 InterPro; IPR002870; Pep_M12B_propep.
 InterPro; IPR001590; Reprolysin.
 InterPro; IPR000130; Zn_MTpeptdse.
 Pfam; PF00200; disintegrin; 1.
 Pfam; PF01421; Reprolysin; 1.
 Pfam; PF01562; Pep_M12B_propep; 1.
 PRINTS; PR00289; DISINTEGRIN.
 ProDom; PD000664; Disintegrin; 1.
 SMART; SM00050; DISIN; 1.
 SMART; PS00215; ADAM_MEPRO; 1.
 PROSITE; PS00427; DISINTEGRIN_1; 1.
 PROSITE; PS00214; DISINTEGRIN_2; 1.
 PROSITE; PS00022; EGF_1; FALSE_NEG.
 PROSITE; PS01186; EGF_2; FALSE_NEG.
 PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
 Signal; Glycoprotein; Zinc; Transmembrane; EGF-like domain.
 SIGNAL 1 16 POTENTIAL.
 FT PROPEP 17 174 REMOVED IN MATURE FORM.
 FT CHAIN 175 735 ADAM 2.
 FT DOMAIN 175 686 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 697 707 POTENTIAL.
 FT DOMAIN 708 735 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 175 382 METALLOPROTEASE-LIKE.
 FT DOMAIN 383 475 DISINTEGRIN-LIKE.
 FT DOMAIN 477 606 CYS-RICH.
 FT DOMAIN 612 686 EGF-LIKE.
 FT DISULFID 287 370 BY SIMILARITY.
 FT DISULFID 329 354 BY SIMILARITY.
 FT DISULFID 445 458 POTENTIAL.
 FT DISULFID 616 627 BY SIMILARITY.
 FT DISULFID 621 633 BY SIMILARITY.
 FT DISULFID 635 644 BY SIMILARITY.
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 220 220 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL).

QY 1 CKGATC 6
 Db 65 CRGSC 70

RESULT 9
 C43B_HUMAN
 ID C43B_HUMAN STANDARD; PRT; 624 AA.
 AC Q9Y5P4; Q9H2S8;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Goodpasture antigen-binding protein (EC 2.7.1.37) (GPBP) (Collagen type IV alpha 3 binding protein).
 GN COL4A3BP.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RX MEDLINE=99230287; PubMed=10212244;
 RA Rava A., Revert F., Navarro S., Saus J.;
 RT "Characterization of a novel type of Serine/Threonine kinase that specifically phosphorylates the human goodpasture antigen.";
 RL J. Biol. Chem. 274:12642-12649(1999).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RX MEDLINE=20568301; PubMed=11007769;
 RA Rava A., Revert-Ros F., Martinez-Martinez P., Navarro S., Rosello E., Vieites B., Granero F., Forteza J., Saus J.;
 RT "Goodpasture antigen-binding protein, the kinase that phosphorylates the Goodpasture antigen, is an alternatively spliced variant implicated in autoimmune pathogenesis.";
 RL J. Biol. Chem. 275:40392-40399(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC Straussberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Phosphorylates on Ser and Thr residues the Goodpasture autoantigen (in vitro). Isoform 2 seems to be less active.
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Interacts with COL4A3.
 CC -!- SUBCELLULAR LOCATION: Not very well defined.
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Delta26/GPBP26; are produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: Widely expressed.
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 START DOMAIN.
 CC -----
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 CC -----
 DR EMBL; AF136450; AAD30288.1; -;
 DR EMBL; AF232930; AAG42046.1; -;
 DR EMBL; BC000102; AAR00102.1; -;
 DR Genew; HGNC:2205; COL4A3BP.
 DR MIM; 604677; -;
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR002913; START.
 DR Pfam; PF00169; PH; 1.
 DR Pfam; PF01852; START; 1.
 DR SMART; SM00233; PH; 1.
 DR SMART; SM00234; START; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 1.
 DR PROSITE; PS50848; START; 1.
 KW Transferase; Coiled coil; Alternative splicing.

FT DOMAIN 23 117 PH.
 FT DOMAIN 263 303 COILED COIL (POTENTIAL).
 FT DOMAIN 389 618 START.
 FT VARSPIC 371 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 624 AA; 70834 MW; A125162492AC5A0E CRC64;

Query Match 83.8%; Score 31; DB 1; Length 624;
 Best Local Similarity 66.7%; Pred. No. 60;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGATC 6
 Db 65 CRGSC 70

RESULT 10
 C43B_MOUSE
 ID C43B_MOUSE STANDARD; PRT; 624 AA.
 AC Q9EQG9; Q9EQG8;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Goodpasture antigen-binding protein (EC 2.7.1.37) (GPBP) (Collagen type IV alpha 3 binding protein).
 GN COL4A3BP.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RX MEDLINE=20568301; PubMed=11007769;
 RA Rava A., Revert-Ros F., Martinez-Martinez P., Navarro S., Rosello E., Vieites B., Granero F., Forteza J., Saus J.;
 RT "Goodpasture antigen-binding protein, the kinase that phosphorylates the Goodpasture antigen, is an alternatively spliced variant implicated in autoimmune pathogenesis.";
 RL J. Biol. Chem. 275:40392-40399(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Geasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- FUNCTION: Phosphorylates on Ser and Thr residues the Goodpasture autoantigen (in vitro). Isoform 2 seems to be less active (by similarity).
 CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
 CC -!- SUBUNIT: Interacts with COL4A3.
 CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/Delta26/GPBP26; are produced by alternative splicing.
 CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 START DOMAIN.
 CC -----
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CC EMBL; U18403; AAA86991.1; -.
CC HSSP; P29972; 1H61.
CC InterPro; IPR000425; MIP_family.
CC Pfam; PF00230; MIP; 1.
CC PRINTS; PR00783; MINTRINSICP.
CC ProDom; PD000295; MIP_family; 1.
CC TIGRFAMs; TIGR00861; MIP; 1.
CC PROSITE; PS00221; MIP; 1.
CC Transport; Transmembrane.
CC SEQUENCE 282 AA; 30260 MW; 42AA96F0EB0F1444 CRC64;

Query Match      83.8%; Score 31; DB 1; Length 282;
Best Local Similarity 83.3%; Pred. No. 30;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
   I:|:|:|
DB 128 CAGAIC 133

RESULT 7
LIPA_AERPE
ID LIPA_AERPE STANDARD; PRT; 295 AA.
AC Q9Y9E3;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable lipoprotein synthetase (LIP-SYN) (Lipoate synthase).
GN LIPA OR APE2344.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;
OC Desulfurococcaceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1;
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1."
RL DNA Res. 6:83-101(1999).
CC -!- FUNCTION: SYNTHESIS OF ALPHA-(+)-LIPIC ACID. IT MAY BE INVOLVED
CC IN THE SULFUR INSERTION CHEMISTRY IN LIPOATE BIOSYNTHESIS (BY
CC SIMILARITY).
CC -!- PATHWAY: Lipoprotein biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: BELONGS TO THE BIOTIN AND LIPOIC ACID SYNTHETASES
CC FAMILY.
CC
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EMBL; AP000064; BAA81357.1; -.
InterPro; IPR003698; Lipoprotein_synth.
Pfam; PF02546; Lipoprotein_synth; 1.
TIGRFAMs; TIGR00510; lipA; 1.
Iron-sulfur; Complete proteome.
METAL 60 60 IRON-SULFUR (POTENTIAL).
METAL 64 64 IRON-SULFUR (POTENTIAL).
METAL 67 67 IRON-SULFUR (POTENTIAL).
SEQUENCE 295 AA; 32435 MW; 2FB10A1A13F4DBFB CRC64;

Query Match      83.8%; Score 31; DB 1; Length 624;
Best Local Similarity 66.7%; Pred. No. 60;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
   I:|:|:|
DB 34 CEGALC 39

RESULT 8
C43B_BOVIN
ID C43B_BOVIN STANDARD; PRT; 624 AA.
AC Q9GKI7; Q9GKI6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Goodpasture antigen-binding protein (EC 2.7.1.37) (GPBP) (Collagen
DE type IV alpha 3 binding protein).
GN COL4A3BP.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=20568301; PubMed=11007769;
RA Rava A., Revert-Ros F., Martinez-Martinez P., Navarro S., Rosello E.,
RA Vieites B., Granero F., Forteza J., Saus J.;
RT "Goodpasture antigen-binding protein, the kinase that phosphorylates
RT the Goodpasture antigen, is an alternatively spliced variant
RT implicated in autoimmune pathogenesis."
RL J. Biol. Chem. 275:40392-40399(2000).
CC -!- FUNCTION: Phosphorylates On Ser and Thr residues the Goodpasture
CC autoantigen (in vitro). Isoform 2 seems to be less active (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -!- SUBUNIT: Interacts with COL4A3.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and
CC 2/Delta26/GPBP26; are produced by alternative splicing.
CC -!- SIMILARITY: CONTAINS 1 PH DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 START DOMAIN.
CC
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Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 299 CKGGVC 304

RESULT 4
VGLG_VSVJO STANDARD; PRT; 517 AA.
AC P04862;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-APR-1990 (Rel. 14, Last annotation update)
DE Spike glycoprotein precursor.
GN G.

OS Vesicular stomatitis virus (serotype New Jersey / strain Ogden).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11283;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83138980; PubMed=6298453;
RA Gallione C.J., Rose J.K.;
RT "Nucleotide sequence of a cDNA clone encoding the entire glycoprotein from the New Jersey serotype of vesicular stomatitis virus.";
RL J. Virol. 46:162-169(1983).
CC -1- FUNCTION: THIS PROTEIN FORMS SPIKES ON THE SURFACE OF THE VIRION. IT IS RESPONSIBLE BOTH FOR THE BINDING OF THE VIRUS TO SUSCEPTIBLE HOST CELLS AND FOR INDUCING THE UPTAKE OF THE VIRUS BY THE CELL. THE INTERACTION BETWEEN THE INTERNAL COMPONENTS OF THE VIRION AND THE PORTION OF THE GLYCOPROTEIN EXPOSED ON THE CYTOPLASMIC FACE OF THE PLASMA MEMBRANE PROBABLY DIRECTS ENVELOPMENT AND VIRUS BUDDING.

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EMBL; V01214; CAA24525.1;
DR PIR; A04118; VGVNVJ.
DR InterPro; IPR001903; Rhabd.glycop.
DR Pfam; PF00974; Rhabd.glycop; 1.
KW Transmembrane; Envelope protein; Glycoprotein; Signal.
FT SIGNAL 1 16
FT CHAIN 17 517 SPIKE GLYCOPROTEIN.
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 340 340 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 517 AA; 58229 MW; A5F0B008B3490194 CRC64;

Query Match 86.5%; Score 32; DB 1; Length 517;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 169 CKGQIC 174

RESULT 5
RL32_CHLMU STANDARD; PRT; 58 AA.
AC O9PLB2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L32.
GN RPWF OR TC0195.
OS Chlamydia muridarum.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
RA "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
RT Nucleic Acids Res. 28:1397-1406(2000).
RL -1- SIMILARITY: BELONGS TO THE L32P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----

EMBL; AE002286; AAF39069.1;
DR TIGR; TC0195;
DR InterPro; IPR002677; Ribosomal_L32p.
DR Pfam; PF01783; Ribosomal_L32p; 1.
DR TIGRFAMs; TIGR01031; rrmF.bact; 1.
KW Ribosomal protein; Complete proteome.
FT INIT_MET 0 BY SIMILARITY.
SQ SEQUENCE 58 AA; 6379 MW; F9D8F77C8730B29D CRC64;

Query Match 83.8%; Score 31; DB 1; Length 58;
Best Local Similarity 66.7%; Pred. No. 7.8;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
Db 24 CSGAVC 29

RESULT 6
AQUA_ATRCA STANDARD; PRT; 282 AA.
ID AC P42767;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Aquaporin.
OS Atriplex canescens (Saltbush).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Caryophyllales; Chenopodiales; Atriplex.
OX NCBI_TaxID=35922;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PURSH NUTT;
RX MEDLINE=95357416; PubMed=7543207;
RA Cairney J., Newton R.J., Funkhouser E.A., Chang S., Hayes D.;
RT "Nucleotide sequence of a cDNA for a water channel protein (aquaporin) homolog from Atriplex canescens (Pursh.) Nutt.";
RL Plant Physiol. 108:1291-1292(1995).
CC -1- FUNCTION: WATER-SPECIFIC CHANNEL.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN FAMILY (TC 1.A.8).
CC -----

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GenCore version 5.1.3

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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:57:44 ; Search time 4.61538 Seconds
(without alignments)
53.919 Million cell updates/sec

Title: US-09-632-748-10

Perfect score: 37

Sequence: 1 CKGAIC 6

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	33	89.2	85	1 IBB3_PHAVU	P81484 phaseolus v
2	33	89.2	85	1 IBB4_PHAVU	P81483 phaseolus v
3	32	86.5	356	1 PA4E_PCOLI	P76081 escherichia
4	32	86.5	517	1 VGLG_VSVJO	P04882 vesicular s
5	31	83.8	58	1 RL32_CHLMO	Q9plb2 chlamydia m
6	31	83.8	282	1 AQUA_ATRCA	P42767 atriplex m
7	31	83.8	295	1 LIPA_AERPE	Q9y9e3 aeropyrum p
8	31	83.8	624	1 C43B_BOVIN	Q9gk17 bos taurus
9	31	83.8	624	1 C43B_HUMAN	Q9y5p4 homo sapien
10	31	83.8	624	1 C43B_MOUSE	Q9eqg9 mus musculus
11	31	83.8	735	1 AD02_HUMAN	Q99965 homo sapien
12	30	81.1	62	1 FER4_METJA	Q57652 methanococc
13	30	81.1	119	1 PA21_ACAAN	P81236 acanthophis
14	30	81.1	285	1 WC2B_ARATH	P43287 arabidopsis
15	30	81.1	285	1 WC2C_ARATH	P30302 arabidopsis
16	30	81.1	286	1 TIPW_LYCES	Q08451 lycopersico
17	30	81.1	286	1 WC1A_ARATH	P43285 arabidopsis
18	30	81.1	286	1 WC1B_ARATH	Q06611 arabidopsis
19	30	81.1	286	1 WC1C_ARATH	P43286 arabidopsis
20	30	81.1	287	1 WC2A_ARATH	P43287 arabidopsis
21	30	81.1	301	1 YF34_SYNV3	P74220 synecocyst
22	30	81.1	323	1 SP55_BACSU	P40870 bacillus su
23	30	81.1	375	1 ADH1_RANPE	P22797 rana perezi
24	30	81.1	729	1 YP65_CABEL	Q09214 caenorhabdi
25	30	81.1	870	1 CLC6_MOUSE	Q35454 mus musculu
26	30	81.1	1276	1 PMP6_CHLPN	Q92899 chlamydia p
27	30	81.1	2871	1 FBN1_MOUSE	Q61554 mus musculu
28	30	81.1	3951	1 VGFL_IBYB	P27920 avian infec
29	29	78.4	112	1 CYC3_DESGI	P00133 desulfovibr
30	29	78.4	157	1 VIEL_FRG3V	P03298 frog virus
31	29	78.4	423	1 GFII_MOUSE	P70338 mus musculu
32	29	78.4	423	1 GFII_RAT	Q07120 rattus norv
33	29	78.4	760	1 TFR1_HUMAN	P02786 homo sapien

RESULT 1
ID IBB3_PHAVU STANDARD; PRT; 85 AA.
AC P81484;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Bowman-Birk type proteinase inhibitor PVI-3(2).
OS Phaseolus vulgaris (Kidney bean) (French bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
OX NCBI_TaxID=3885;
RN [1]
RP SEQUENCE.
RC STRAIN=cv. Borlotto;
RX MEDLINE=93262881; PubMed=8493818;
RA Funk A., Weder J.K., Belitz H.-D.;
RT "Primary structures of proteinase inhibitors from Phaseolus vulgaris
var. nanus (cv. Borlotto).";
RL Lebensm. Unters. Forsch. 196;343-350(1993).
CC -|- SIMILARITY: BELONGS TO THE BOWMAN-BIRK SERINE PROTEASE INHIBITORS
CC FAMILY.
DR HSSP; P01055; 1BBI.
DR InterPro; IPR000877; Bowman-Birk_leg.
DR Pfam; PF00228; Bowman-Birk_leg; 1.
DR ProDom; PD002168; Bowman-Birk_leg; 1.
DR SMART; SM00269; BowB; 1.
DR PROSITE; PS00281; BOWMAN_BIRK; FALSE_NEG.
KW Serine protease inhibitor.
FT ACT_SITE 29 30 INTERACTION WITH TRYPSIN (BY SIMILARITY).
FT ACT_SITE 56 57 INTERACTION WITH CHYMOTRYPSIN (BY
SIMILARITY).
FT DISULFID 21 75 BY SIMILARITY.
FT DISULFID 22 37 BY SIMILARITY.
FT DISULFID 25 71 BY SIMILARITY.
FT DISULFID 27 35 BY SIMILARITY.
FT DISULFID 45 52 BY SIMILARITY.
FT DISULFID 49 64 BY SIMILARITY.
FT DISULFID 54 62 BY SIMILARITY.
SQ SEQUENCE 85 AA; 9217 MW; 32DFB3DF2C86300C CRC64;

Query Match 89.2%; Score 33; DB 1; Length 85;
Best Local Similarity 83.3%; Pred. No. 4.4;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
||| ||
Db 49 CKGCIC 54

RESULT 2
ID IBB4_PHAVU STANDARD; PRT; 85 AA.
AC P81483;
DT 15-DEC-1998 (Rel. 37, Created)

P51797 homo sapien
P98133 bos taurus
P35555 homo sapien
Q9CV36 sus scrofa
P38608 agriosphodr
P5817 diguetia ca
P21789 cerastes ce
P81458 daboia russ
O62939 pinus thunb
P48376 caenorhabdi
O83715 treponema p
Q9UX10 sulfolobus

DR EMBL; AL035395; CAB37612.1; -.
DR FlyBase: FBgn0028746; EG:140G11.3.
SQ SEQUENCE 99 AA; 11150 MW; 0BF00050D1F11758 CRC64;

Query Match 86.5%; Score 32; DB 5; Length 99;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
||| :|
Db 51 CKGGVC 56

Search completed: November 9, 2002, 14:03:03
Job time : 16.9231 secs

SQ SEQUENCE 627 AA; 71928 MW; C909B8878B1AC0F6 CRC64;

Query Match 89.2%; Score 33; DB 12; Length 627;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 407 CKGSVC 412

RESULT 13

ID Q8V396

AC Q8V396 PRELIMINARY; PRT; 627 AA.

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE Nonstructural protein NS.

GN NS.

OS goose parvovirus.

OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.

OX NCBI_TaxID=38251;

RN [1]

RC STRAIN=GPV-YG;

RA Ge Y., You Y., Xu Q.;

RT "Analysis of the major open reading frames' nucleotide sequences in

RT Goose parvovirus GPV-YG strain isolated in China."

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF416726; AAL37721.1; -

DR InterPro: IPR001257; Parvo.NS1.

DR Pfam: PF01057; Parvo.NS1.

SQ SEQUENCE 627 AA; 71943 MW; 4301A125FCACA7D1 CRC64;

Query Match

Best Local Similarity 89.2%; Score 33; DB 12; Length 627;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 407 CKGSVC 412

RESULT 14

ID Q8SVT4

AC Q8SVT4 PRELIMINARY; PRT; 69 AA.

DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)

DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)

DE RE346699

GN EG:140G11.3

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RC STRAIN=BERKELEY;

RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,

RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,

RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,

RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,

RA Celniker S.;

RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY071325; AAL48947.1; -

SQ SEQUENCE 69 AA; 8120 MW; F5CE3B840B3DAB7F CRC64;

Query Match

Best Local Similarity 86.5%; Score 32; DB 5; Length 69;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6

Db 407 CKGSVC 412

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

RESULT 15

ID Q97172

AC Q97172 PRELIMINARY; PRT; 99 AA.

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)

DE EG:140G11.3 protein.

GN EG:140G11.3 OR CG4015 OR CG18508.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RC STRAIN=BERKELEY;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,

RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foslter C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RC STRAIN=BERKELEY;

RA Borkova D., Minana B., Kafatos F.C.;

RA "Sequencing the distal X chromosome of Drosophila melanogaster.";

RT Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

RN [3]

RC STRAIN=BERKELEY;

RA Benos P.;

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003426; AAF45849.1; -

DR EMBL; U34761; AAA75285.1; -
 DR InterPro; IPR001257; Parvo_NSL1.
 DR Pfam; PF01057; Parvo_NSL1; 1.
 FT NON_TER 1
 SQ SEQUENCE 461 AA; 52594 MW; 7D07F2672EB834EB CRC64;

Query Match 89.2%; Score 33; DB 12; Length 461;
 Best Local Similarity 66.7%; Pred. No. 32;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CKGAIC 6
 |||::|
 Db 241 CKGSVC 246

RESULT 9

Q9P8C2
 ID Q9P8C2 PRELIMINARY; PRT; 511 AA.

AC Q9P8C2;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Arylsulfatase (EC 3.1.6.1) (Fragment).
 GN ARS
 OS Colletotrichum gloeosporioides f. sp. malvae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Phyllachorales; Phyllachoraceae;
 OC Glomerella.
 OX NCBI_TaxID=96478;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Goodwin P., Li J., Jin S.;
 RT "Evidence for sulfate derepression of an arylsulfatase gene of
 RT Colletotrichum gloeosporioides f. sp. malvae during infection of round-
 RT leaved mallow, Malva pusilla."
 RL Physiol. Mol. Plant Pathol. 57:169-176(2000).
 DR EMBL; AJ271152; CAB70953.1; -
 DR InterPro; IPR000917; Sulfatase.
 DR Pfam; PF00884; Sulfatase; 1.
 KW Hydrolase.
 FT NON_TER 1
 SQ SEQUENCE 511 AA; 57405 MW; E9AC0739E3E0D69B CRC64;

Query Match 89.2%; Score 33; DB 3; Length 511;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CKGAIC 6
 |||::|
 Db 436 CKGSVC 441

RESULT 10

Q83288
 ID Q83288 PRELIMINARY; PRT; 626 AA.

AC Q83288;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE NS1 protein.
 GN NSL.
 OS Muscovy duck parvovirus.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxID=37325;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zadori Z., Erdel J., Nagy J., Kisari J.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X75093; CAA52983.1; -
 DR InterPro; IPR001257; Parvo_NSL1.
 DR Pfam; PF01057; Parvo_NSL1; 1.
 SQ SEQUENCE 626 AA; 71683 MW; 0A088CA3B0F5CB1 CRC64;

Query Match 89.2%; Score 33; DB 12; Length 626;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CKGAIC 6
 |||::|
 Db 406 CKGSVC 411

RESULT 11

Q65443
 ID Q65443 PRELIMINARY; PRT; 627 AA.

AC Q65443;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE REP protein.
 GN REP.
 OS Barbarie duck parvovirus.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxID=39118;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-PM;
 RX MEDLINE=96010229; PubMed=7571426;
 RA Zadori Z., Stefancsik R., Rauch T., Kisary J.;
 RT "Analysis of the complete nucleotide sequences of goose and muscovy
 RT duck parvoviruses indicates common ancestral origin with adeno-
 RT associated virus 2."
 RL Virology 212:562-573(1995).
 DR EMBL; U22967; AAA83224.1; -
 DR InterPro; IPR001257; Parvo_NSL1.
 DR Pfam; PF01057; Parvo_NSL1; 1.
 SQ SEQUENCE 627 AA; 71812 MW; C359097CDDA967DC CRC64;

Query Match 89.2%; Score 33; DB 12; Length 627;
 Best Local Similarity 66.7%; Pred. No. 41;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 CKGAIC 6
 |||::|
 Db 407 CKGSVC 412

RESULT 12

Q67665
 ID Q67665 PRELIMINARY; PRT; 627 AA.

AC Q67665;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE REP.
 GN REP.
 OS goose parvovirus.
 OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
 OX NCBI_TaxID=38251;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VIRULENT B;
 RX MEDLINE=96010229; PubMed=7571426;
 RA Zadori Z., Stefancsik R., Rauch T., Kisary J.;
 RT "Analysis of the complete nucleotide sequences of goose and muscovy
 RT duck parvoviruses indicates common ancestral origin with adeno-
 RT associated virus 2."
 RL Virology 212:562-573(1995).
 RN [2]
 RP SEQUENCE FROM N.A.

RC STRAIN-VIRULENT B;
 RA Zadori Z.;
 RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U25749; AAA83229.1; -
 DR InterPro; IPR001257; Parvo_NSL1.
 DR Pfam; PF01057; Parvo_NSL1; 1.

```

RP SEQUENCE FROM N.A.
RA German Neurospora genome project;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL356834; CAB92713.2; -.
KW Hypothetical protein.
SQ SEQUENCE 137 AA; 14743 MW; 35FF23569D4616AB CRC64;

Query Match      89.2%; Score 33; DB 3; Length 137;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
   ||| ||
Db 93 CKGGIC 98

RESULT 5
Q8T8W9 PRELIMINARY; PRT; 260 AA.
AC Q8T8W9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 60S ribosomal protein L3.
GN AT19932p.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY075239; AAL68106.1; -.
SQ SEQUENCE 260 AA; 29048 MW; A254A62E23471A51 CRC64;

Query Match      89.2%; Score 33; DB 5; Length 260;
Best Local Similarity 66.7%; Pred. No. 19;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
   ||| ||
Db 110 CKGSVC 115

RESULT 6
Q9F7P2 PRELIMINARY; PRT; 270 AA.
AC Q9F7P2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE Predicted formamidopyrimidine-DNA glycosylase.
OS uncultured proteobacterium EBAC31A08.
OC Bacteria; Proteobacteria; environmental samples.
OX NCBI_TaxID=133804;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=20445260; PubMed=10988064;
RA Beja O., Aravind L., Koonin E.V., Suzuki M.T., Hadd A., Nguyen L.P.,
RA Jovanovich S.B., Gates C.M., Feldman R.A., Spudich J.L., Spudich E.N.,
RA DeLong E.F.;
RT "Bacterial rhodopsin: evidence for a new type of phototrophy in the
RT Sea.";
RL Science 289:1902-1906(2000).
DR EMBL; AF279106; AAG10477.1; -.
DR HSSP; O50606; 1EE8.
DR InterPro; IPR000191; Fapy_DNA_glyco.

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DR Pfam; PF01149; Fapy_DNA_glyco; 1.
DR ProDom; PD003680; Fapy_DNA_glyco; 1.
DR TIGRFAMs; TIGR00577; fpg; 1.
SQ SEQUENCE 270 AA; 30736 MW; 44B3306AF754DDD8 CRC64;

Query Match      89.2%; Score 33; DB 2; Length 270;
Best Local Similarity 83.3%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CKGAIC 6
   ||| ||
Db 248 CKGTIC 253

RESULT 7
Q8SQI3 PRELIMINARY; PRT; 383 AA.
AC Q8SQI3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DE 60S ribosomal protein L3.
GN ECU03.1220 OR ECU09.1000.
OS Encephalitozoon cuniculi.
OC Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
OX NCBI_TaxID=6035;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=GB-M1;
RA Genoscope;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=GB-M1;
RX MEDLINE=21576510; PubMed=11719806;
RA Katinka M.D., Duprat S., Cornillot E., Metenier G., Thomarat F.,
RA Prensier G., Barbe V., Peyretailade E., Brottier P., Wincker P.,
RA Delbac F., El Alaoui H., Peyret P., Saurin W., Gouy M.,
RA Weissenbach J., Vivares C.P.;
RT "Genome sequence and gene compaction of the eukaryote parasite
RT Encephalitozoon cuniculi.";
RL Nature 414:450-453(2001).
DR EMBL; AL590443; CAD26265.1; -.
DR EMBL; AL590451; CAD27073.1; -.
SQ SEQUENCE 383 AA; 42475 MW; 677047CE70BC118D CRC64;

Query Match      89.2%; Score 33; DB 5; Length 383;
Best Local Similarity 66.7%; Pred. No. 27;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6
   ||| ||
Db 134 CKGSVC 139

RESULT 8
Q67671 PRELIMINARY; PRT; 461 AA.
AC Q67671;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NS1 (Fragment).
OS goose parvovirus.
OC Viruses; ssDNA viruses; Parvoviridae; Parvovirinae; Parvovirus.
OX NCBI_TaxID=38251;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHM 319;
RX MEDLINE=95343541; PubMed=7618268;
RA Brown K.E., Green S.W., Young N.S.;
RT "Goose parvovirus--an autonomous member of the dependovirus genus?";
RL Virology 210:283-291(1995).

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DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-MAR-2002 (TREMREL. 20, Last annotation update)
 DE Guinea pig PH-30 beta precursor.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RN SEQUENCE OF 383-735 FROM N.A.
 RC TISSUE=TESTIS;
 RX MEDLINE=92204234; PubMed=1552944;
 RA Blobel C.P., Wolfsberg T.G., Turck C.W., Myles D.G., Primakoff P.,
 RA White J.M.;
 RA "A potential fusion peptide and an integrin ligand domain in a protein
 RT active in sperm-egg fusion.";
 RL Nature 356:248-252(1992).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Wolfsberg T.G., Bazan J.F., Blobel C.P., Myles D.G., Primakoff P.,
 RA White J.M.;
 RA "The precursor region of a protein active in sperm-egg fusion contains
 RT a metalloprotease and a disintegrin domain: Structural, functional,
 RT and evolutionary implications.";
 RL Proc. Natl. Acad. Sci. U.S.A. 0:0-0(1993).
 RN [3]
 RN SEQUENCE FROM N.A.
 RC TISSUE=TESTIS;
 RA Wolfsberg T.G.;
 RL Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z11720; CAA77784.1; -;
 DR HSP; P18619; IFLV.
 DR MEROPS; M12.950; -;
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR002870; Pep.M12B_propep.
 DR InterPro; IPR001590; Reprolysin.
 DR Pfam; PF00200; disintegrin; 1.
 DR Pfam; PF01582; Pep.M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR ProDom; PD00664; Disintegrin; 1.
 DR SMART; SM00050; DISIN; 1.
 DR SMART; SM00181; EGF; 1.
 DR PROSITE; PS0215; ADAM_MEPRO; 1.
 DR PROSITE; PS0427; DISINTEGRIN_1; 1.
 DR PROSITE; PS0214; DISINTEGRIN_2; 1.
 KW SIGNAL.
 FT CHAIN 1 15 POTENTIAL.
 FT CHAIN 16 735 PH-30 PRO-BETA FOUND ON TESTICULAR
 FT CHAIN 16 735 SPERMATOGENIC CELLS.
 FT CHAIN 383 735 MATURE PH-30 BETA PRESENT ON
 FT CHAIN 383 735 FERTILIZATION-COMPETENT SPERM.
 SQ SEQUENCE 735 AA; 81904 MW; 7535FC39F44FB645 CRC64;
 Query Match 91.9%; Score 34; DB 11; Length 735;
 Best Local Similarity 83.3%; Pred. No. 29;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CKGAIC 6
 Db 331 CKGAIC 336
 RESULT 3
 Q9LQT3 PRELIMINARY; PRT; 125 AA.
 AC Q9LQT3;
 DT 01-OCT-2000 (TREMREL. 15, Created)
 DT 01-OCT-2000 (TREMREL. 15, Last sequence update)
 DT 01-JUN-2001 (TREMREL. 17, Last annotation update)
 DE T4012.4.
 OS Arabidopsis thaliana (Mouse-ear cross).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Chao Q., Shinn P., Brooks S., Buehler E., Dunn P., Khan S., Kim C.,
 RA Walker M., Brooks S., Altafi H., Araujo R., Conn L., Conway A.B.,
 RA Gonzalez A., Hansen N.F., Huizar L., Kremenetskaia I., Lenz C., Li J.,
 RA Liu S., Luros S., Rowley D., Schwartz J., Toriumi M., Vysotskaia V.,
 RA Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC T4012 from chromosome
 RT I.";
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RN SEQUENCE FROM N.A.
 RA Chao Q., Brooks S., Buehler E., Johnson-Hopson C., Khan S., Kim C.,
 RA Shinn P., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L.,
 RA Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsy N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A.,
 RA Ecker J.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RN SEQUENCE FROM N.A.
 RA Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsy N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC007396; AAF26753.1; -;
 SQ SEQUENCE 125 AA; 13323 MW; DE3F0E698B107CD7 CRC64;
 Query Match 89.2%; Score 33; DB 10; Length 125;
 Best Local Similarity 83.3%; Pred. No. 10;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 CKGAIC 6
 Db 94 CKGGIC 99
 RESULT 4
 Q9P4Y2 PRELIMINARY; PRT; 137 AA.
 ID Q9P4Y2;
 AC Q9P4Y2;
 DT 01-OCT-2000 (TREMREL. 15, Created)
 DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
 DT 01-DEC-2001 (TREMREL. 19, Last annotation update)
 DE Hypothetical 14.7 kDa protein.
 GN B11822.100.
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RN SEQUENCE FROM N.A.
 RA Schulte U., Algn V., Hoheisel J., Brandt P., Fartmann B., Holland R.,
 RA Nyakatura G., Mewes H.W., Mannhaupt G.;
 RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:04 ; Search time 15.9231 Seconds
(without alignments)
77.641 Million cell updates/sec

Title: US-09-632-748-10
Perfect score: 37
Sequence: 1 CKGAIC 6

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	94.6	221	17 Q8ZYU8	Q8zyu8 pyrobaculum
2	34	91.9	735	11 Q60411	Q60411 cavia porce
3	33	89.2	125	10 Q9LQT3	Q9lqt3 arabidopsis
4	33	89.2	137	3 Q9P4Y2	Q9p4y2 neurospora
5	33	89.2	260	5 Q8T8W9	Q8t8w9 drosophila
6	33	89.2	270	2 Q9F7P2	Q9f7p2 uncultured
7	33	89.2	383	5 Q8SQI3	Q8sqi3 encephalito
8	33	89.2	461	12 Q67671	Q67671 goose parvo
9	33	89.2	511	3 Q9P8C2	Q9p8c2 collettotric
10	33	89.2	626	12 Q83288	Q83288 muscovy duc
11	33	89.2	627	12 Q65443	Q65443 barbarie du
12	33	89.2	627	12 Q67665	Q67665 goose parvo
13	33	89.2	627	12 Q8V396	Q8v396 goose parvo
14	32	86.5	69	5 Q8SVT4	Q8svt4 drosophila
15	32	86.5	98	5 Q97172	Q97172 drosophila
16	32	86.5	245	16 Q8YEK7	Q8yek7 bruceella me

ALIGNMENTS

RESULT 1

Q8ZYU8 PRELIMINARY; PRT; 221 AA.
AC Q8ZYU8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein PAE0613.
GN PAE0613
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX PubMed=11792869;
RA Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT aerophilum";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009775; AAL62895.1; .
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 221 AA; 24620 MW; C5822D09DF808C CRC64;

Query Match 94.6%; Score 35; DB 17; Length 221;
Best Local Similarity 83.3%; Pred. No. 6.1;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 CKGAIC 6

|||||
Db 157 CKGALC 162

RESULT 2

Q60411 PRELIMINARY; PRT; 735 AA.
AC Q60411;

Q9IG71 vesicular s
Q9IG68 vesicular s
Q9IG64 vesicular s
Q9IG62 vesicular s
Q9IG59 vesicular s
Q9IG57 vesicular s
Q9IG55 vesicular s
Q9IG53 vesicular s
Q9IG51 vesicular s
Q9IG49 vesicular s
Q9IG47 vesicular s
Q8X573 ralstonia s
Q93Jc1 streptomyce
Q9XZ28 litomosoides
Q96K68 homo sapien
Q9DH91 vesicular s
Q9DZ28 vesicular s
Q9DGZ8 vesicular s
Q9DG27 vesicular s
Q89009 vesicular s
Q89010 vesicular s
Q89011 vesicular s
Q89012 vesicular s
Q89013 vesicular s
Q89014 vesicular s
Q89015 vesicular s
Q89016 vesicular s
Q89017 vesicular s
Q89018 vesicular s

Job time : 14.0769 secs

TELEFAX: (415) 494-0792
TELEX: 706141 MRSNFOERS SFO
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-753-642-2

Query Match 59.6%; Score 34; DB 3; Length 119;
Best Local Similarity 87.5%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
|||||
Db 29 ATDIKGKE 36

RESULT 15
US-07-979-630-1
; Sequence 1, Application US/07979630
; Patent No. 5488099
; GENERAL INFORMATION:
; APPLICANT: Persson, et al.
; TITLE OF INVENTION: Multifunctional Neurotrophic Factors
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/979,630
; FILING DATE: 20-NOV-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,369
; FILING DATE: 06-MAR-1992
; NAME:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler Ph.D., Gail M.
; REGISTRATION NUMBER: 32,143
; REFERENCE/DOCKET NUMBER: REG 41
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914-347-7000
; TELEFAX: 914-347-2113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-07-979-630-1

Query Match 59.6%; Score 34; DB 1; Length 120;
Best Local Similarity 87.5%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
|||||
Db 28 ATDIKGKE 35

Search completed: November 9, 2002, 14:04:23

Query Match 59.6%; Score 34; DB 1; Length 12;
Best Local Similarity 87.5%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
| | | | |
Db 4 ATDIKGKE 11

RESULT 12

US-08-300-044-1
; Sequence 1, Application US/08300044
; Patent No. 5705617
; GENERAL INFORMATION:
; APPLICANT: Persson, Hakan B. et al.
; TITLE OF INVENTION: Neurotrophic Factors Having Altered
; TITLE OF INVENTION: Receptor Binding Specificities
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
; STREET: 777 Old Saw Mill River Road
; CITY: Tarrytown
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10591-6707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/300,044
; FILING DATE: 02-SEP-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/847,369
; FILING DATE: 06-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kempler, Gail M./Misrock, S. Leslie
; REGISTRATION NUMBER: 32,143/18,872
; REFERENCE/DOCKET NUMBER: 6526-097
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 914 347-7000
; TELEFAX: 914 347-2113
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-300-044-1

Query Match 59.6%; Score 34; DB 1; Length 12;
Best Local Similarity 87.5%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
| | | | |
Db 4 ATDIKGKE 11

RESULT 13

US-08-300-044-2
; Sequence 2, Application US/08300044
; Patent No. 5705617
; GENERAL INFORMATION:
; APPLICANT: Persson, Hakan B. et al.
; TITLE OF INVENTION: Neurotrophic Factors Having Altered
; TITLE OF INVENTION: Receptor Binding Specificities
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Regeneron Pharmaceuticals, Inc.

STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/300,044
FILING DATE: 02-SEP-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,369
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M./Misrock, S. Leslie
REGISTRATION NUMBER: 32,143/18,872
REFERENCE/DOCKET NUMBER: 6526-097
TELECOMMUNICATION INFORMATION:
TELEPHONE: 914 347-7000
TELEFAX: 914 347-2113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-300-044-2

Query Match 59.6%; Score 34; DB 1; Length 12;
Best Local Similarity 87.5%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
| | | | |
Db 4 ATDIKGKE 11

RESULT 14

US-08-753-642-2
; Sequence 2, Application US/08753642
; Patent No. 6063757
; GENERAL INFORMATION:
; APPLICANT: URISO, RICHARD G.
; TITLE OF INVENTION: WOUND TREATMENT METHOD WITH NERVE GROWTH
; TITLE OF INVENTION: FACTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/753,642
FILING DATE: 27-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, GLADYS H.
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 32718-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600

APPLICANT: CUELLO, Claudio A.
TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: KLAUBER & JACKSON
CITY: Hackensack
STATE: N.J.
COUNTRY: U.S.A.
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-AUG-1996
PRIORITY APPLICATION NUMBER: US/08/696,854B
PRIORITY APPLICATION DATA:
FILING DATE: 07-FEB-1995
PRIORITY APPLICATION NUMBER: WO PCT/CA95/00059
PRIORITY APPLICATION DATA:
FILING DATE: 07-FEB-1994
FILING DATE: 07-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON, David A.
REGISTRATION NUMBER: 26,742
TELEPHONE: (201) 487-5800
TELEFAX: (201) 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: one-of (1, 10)
OTHER INFORMATION: /note= "Xaa is any uncharged amino acid
OTHER INFORMATION: or hydropathic amino acid"
US-08-696-854B-2

Query Match 59.6%; Score 34; DB 3; Length 10;
Best Local Similarity 85.7%; Pred. No. 2.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 DIKGAC 10
Db 3 DIKGEC 9

RESULT 10
US-07-847-369-1
Sequence 1, Application US/07847369
Patent No. 5349055
GENERAL INFORMATION:
APPLICANT: Persson, Hakan B. et al.
TITLE OF INVENTION: Neurotrophic Factors Having Altered
RECEPTOR BINDING SPECIFICITIES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920306
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M./Misrock, S. Leslie
REGISTRATION NUMBER: 32,143/18,872
REFERENCE/DOCKET NUMBER: 6526-097
TELEPHONE: 914 347-7000
TELEFAX: 914 347-2113
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-847-369-1

Query Match 59.6%; Score 34; DB 1; Length 12;
Best Local Similarity 87.5%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGA 9
Db 4 ATDIKGA 11

RESULT 11
US-07-847-369-2
Sequence 2, Application US/07847369
Patent No. 5349055
GENERAL INFORMATION:
APPLICANT: Persson, Hakan B. et al.
TITLE OF INVENTION: Neurotrophic Factors Having Altered
RECEPTOR BINDING SPECIFICITIES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Regeneron Pharmaceuticals, Inc.
STREET: 777 Old Saw Mill River Road
CITY: Tarrytown
STATE: New York
COUNTRY: U.S.A.
ZIP: 10591-6707
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 19920306
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Kempler, Gail M./Misrock, S. Leslie
REGISTRATION NUMBER: 32,143/18,872
REFERENCE/DOCKET NUMBER: 6526-097
TELEPHONE: 914 347-7000
TELEFAX: 914 347-2113
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-847-369-2

RESULT 6

PCT-US93-06093-2
; Sequence 2, Application PC/TUS9306093
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/06093
; FILING DATE: 19930625
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2609
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1124 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-06093-2

Query Match 61.4%; Score 35; DB 5; Length 1124;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAC 10
||| ||| |
Db 289 CATGKWLQC 298

RESULT 7

US-09-462-136-9
; Sequence 9, Application US/09462136
; Patent No. 6426198
; GENERAL INFORMATION:
; APPLICANT: Carstea, et al.
; TITLE OF INVENTION: Genes for Niemann-Pick Type C Disease
; FILE REFERENCE: 4239-53894
; CURRENT APPLICATION NUMBER: US/09/462,136
; CURRENT FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/13862
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/051,682
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 9
; LENGTH: 1296
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-462-136-9

Query Match 60.5%; Score 34.5; DB 4; Length 1296;
Best Local Similarity 53.8%; Pred. No. 2.8e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 CAT---DIKGAC 10
| | | | | | | |
Db 1006 CVTLGIDVKGAC 1018

RESULT 8

US-08-696-854B-5
; Sequence 5, Application US/08696854B
; Patent No. 6017878
; GENERAL INFORMATION:
; APPLICANT: SARAGOV, Uri H.
; APPLICANT: Lesauteur, Lynne
; APPLICANT: CUELLO, Claudio A.
; TITLE OF INVENTION: NERVE GROWTH FACTOR STRUCTURAL ANALOGS
; TITLE OF INVENTION: AND THEIR USES
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: KLAUBER & JACKSON
; STREET: Continental Plaza, 411 Hackensack Avenue
; CITY: Hackensack
; STATE: N.J.
; COUNTRY: U.S.A.
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,854B
; FILING DATE: 07-AUG-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA95/00059
; FILING DATE: 07-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9402331.4
; FILING DATE: 07-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: JACKSON, David A.
; REGISTRATION NUMBER: 26,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 487-5800
; TELEFAX: (201) 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-696-854B-5

Query Match 59.6%; Score 34; DB 3; Length 9;
Best Local Similarity 87.5%; Pred. No. 2e+05;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 ATDIKGAE 9
| | | | | | |
Db 1 ATDIKGKE 8

RESULT 9

US-08-696-854B-2
; Sequence 2, Application US/08696854B
; Patent No. 6017878
; GENERAL INFORMATION:
; APPLICANT: SARAGOV, Uri H.
; APPLICANT: Lesauteur, Lynne

Db 437 CATGKGVDC 446
||| || :|

RESULT 2

US-08-899-232-4
; Sequence 4, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 2703
; TYPE: PRT
; ORGANISM: Drosophila sp.
US-08-899-232-4

Query Match 66.7%; Score 38; DB 4; Length 2703;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
||| || :|
Db 437 CATGKGVDC 446

RESULT 3

US-09-590-656-2
; Sequence 2, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A
; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 704
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-2

Query Match 61.4%; Score 35; DB 4; Length 704;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
||| || :|
Db 289 CATGWRGLQC 298

RESULT 4

US-09-590-656-1
; Sequence 1, Application US/09590656
; Patent No. 6413932
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Borges, Luis G.
; APPLICANT: Fanslow, III, William C.
; TITLE OF INVENTION: TEK ANTAGONISTS
; FILE REFERENCE: 2900-A

; CURRENT APPLICATION NUMBER: US/09/590,656
; CURRENT FILING DATE: 2000-06-07
; PRIOR APPLICATION NUMBER: 60/137,889
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 977
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-590-656-1

Query Match 61.4%; Score 35; DB 4; Length 977;
Best Local Similarity 60.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
||| || :|
Db 289 CATGWRGLQC 298

RESULT 5

US-08-323-474-2
; Sequence 2, Application US/08323474
; Patent No. 5447860
; GENERAL INFORMATION:
; APPLICANT: Ziegler, Steven F.
; TITLE OF INVENTION: NOVEL TYROSINE KINASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,474
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/905,600
; FILING DATE: 26-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2609
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1124 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-323-474-2

Query Match 61.4%; Score 35; DB 1; Length 1124;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
||| || :|
Db 289 CATGWRGLQC 298

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 9, 2002, 13:59:59 ; Search time 13.0769 Seconds
(without alignments)
22.500 Million cell updates/sec

Title: US-09-632-748-9

Perfect score: 57

Sequence: 1 CATDIKGAEC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	66.7	2703	1	US-08-185-432-19
2	38	66.7	2703	4	US-08-899-232-4
3	35	61.4	704	4	US-09-590-656-2
4	35	61.4	977	4	US-09-590-656-1
5	35	61.4	1124	1	US-08-323-474-2
6	35	61.4	1124	5	PCT-US93-06093-2
7	34.5	60.5	1296	4	US-09-462-136-9
8	34	59.6	9	3	US-08-696-854B-5
9	34	59.6	10	3	US-08-696-854B-2
10	34	59.6	12	1	US-07-847-369-1
11	34	59.6	12	1	US-07-847-369-2
12	34	59.6	12	1	US-08-300-044-1
13	34	59.6	12	1	US-08-300-044-2
14	34	59.6	119	3	US-08-753-642-2
15	34	59.6	120	1	US-07-979-630-1
16	34	59.6	120	1	US-08-440-049-1
17	34	59.6	120	1	US-08-440-049-3
18	34	59.6	120	2	US-08-441-513A-1
19	34	59.6	120	2	US-08-441-513A-3
20	34	59.6	120	3	US-08-970-865-2
21	34	59.6	120	3	US-08-970-865-3
22	34	59.6	120	3	US-08-581-662-31
23	34	59.6	120	4	US-09-363-573-2
24	34	59.6	120	4	US-09-363-573-3
25	34	59.6	120	4	US-08-845-541B-1
26	34	59.6	120	4	US-08-845-541B-3
27	34	59.6	120	4	US-08-845-541B-4

28	34	59.6	120	4	US-08-845-541B-5	Sequence 5, Appli
29	34	59.6	120	4	US-08-845-541B-7	Sequence 7, Appli
30	34	59.6	120	4	US-08-845-541B-8	Sequence 8, Appli
31	34	59.6	120	4	US-08-845-541B-10	Sequence 10, Appli
32	34	59.6	120	4	US-08-845-541B-11	Sequence 11, Appli
33	34	59.6	120	4	US-08-845-541B-12	Sequence 12, Appli
34	34	59.6	120	4	US-08-845-541B-17	Sequence 17, Appli
35	34	59.6	120	4	US-08-845-541B-18	Sequence 18, Appli
36	34	59.6	120	4	US-08-845-541B-19	Sequence 19, Appli
37	34	59.6	120	4	US-08-845-541B-20	Sequence 20, Appli
38	34	59.6	120	4	US-08-845-541B-21	Sequence 21, Appli
39	34	59.6	120	4	US-09-066-065A-1	Sequence 1, Appli
40	34	59.6	120	4	US-09-066-065A-3	Sequence 3, Appli
41	34	59.6	120	4	US-09-066-065A-4	Sequence 4, Appli
42	34	59.6	120	4	US-09-066-065A-5	Sequence 5, Appli
43	34	59.6	120	4	US-09-066-065A-7	Sequence 7, Appli
44	34	59.6	120	4	US-09-066-065A-8	Sequence 8, Appli
45	34	59.6	120	4	US-09-066-065A-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-185-432-19
; Sequence 19, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEx PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDWARDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2703 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-185-432-19

Query Match 66.7%; Score 38; DB 1; Length 2703;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10

QY 1 CATDIKGAEC 10
| | | | |
Db 178 CDLDFKGTQC 187

RESULT 13

US-09-305-856B-6
; Sequence 6, Application US/09305856B
; Patent No. US20020061518A1
; GENERAL INFORMATION:
; APPLICANT: Penay, Laura
; APPLICANT: Galvin, Margaret
; TITLE OF INVENTION: Genotyping the Human
; FILE REFERENCE: UDP-Glucuronosyltransferase 1 (UGT1) Gene
; CURRENT APPLICATION NUMBER: 4389-7 (formerly SEQ-17C1P)
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: US/09/305,856B
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 60/084,807
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-305-856B-6

Query Match 59.6%; Score 34; DB 10; Length 289;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
| | | | |
Db 178 CDLDFKGTQC 187

RESULT 14

US-09-305-856B-8
; Sequence 8, Application US/09305856B
; Patent No. US20020061518A1
; GENERAL INFORMATION:
; APPLICANT: Penny, Laura
; APPLICANT: Galvin, Margaret
; TITLE OF INVENTION: Genotyping the Human
; FILE REFERENCE: UDP-Glucuronosyltransferase 1 (UGT1) Gene
; CURRENT APPLICATION NUMBER: 4389-7 (formerly SEQ-17C1P)
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: US/09/305,856B
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 289
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-305-856B-8

Query Match 59.6%; Score 34; DB 10; Length 289;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 10
| | | | |
Db 178 CDLDFKGTQC 187

RESULT 15

US-09-919-497-53
; Sequence 53, Application US/09919497
; Patent No. US20020106662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.

; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0801/7225
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/221,735
; PRIOR FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 53
; LENGTH: 373
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-919-497-53

Query Match 59.6%; Score 34; DB 10; Length 373;
Best Local Similarity 55.6%; Pred. No. 32;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CATDIKGAEC 9
| | | | |
Db 151 CCTDLRGLLE 159

Search completed: November 9, 2002, 14:11:55
Job time : 6.15385 secs